

09885-06101

5

10

Field of the Invention

15

25

30

receptors to provide ligand-binding or signal-transducing domains thereof, and construction of fusion sensory receptor proteins will separate the diverse physiological functions associated with sensory perception at the level of ligand-receptor binding. Furthermore, novel "primary sensants" that are identified and isolated by the methods described herein may be used to further define the function of the cognate sensory receptor by uniquely enhancing or, in the alternative, blocking stimulation of sensory receptors with a single ligand-binding domain.

The present invention addresses the need for better understanding of these ligand-receptor interactions by using a large set of identified sensory receptors. Even if the receptor set used is incomplete (*i.e.*, a partial set of all sensory receptors encoded in the genome), a large number of sensants will be detected. Moreover, redundancy in the chemical structures recognized by the sensory receptors or combinatorial processing of signals from different sensory receptors would allow broad coverage of chemically diverse sensants (*e.g.*, by selection of a representative class of sensory receptors). Also provided are, *inter alia*, methods for utilizing such sensory receptors and biosensors to simulate sensory perception. To analyze ligand-receptor interactions and their effects on cell signaling and the processing of those signals in sensory perception, specific sensants and their cognate receptor complexes are detected, identified, and measured under binding conditions. Fragrances and flavorings can be detected, identified, measured, and/or custom designed by the methods herein described. In addition, drugs that incorporate artificial odors and/or tastes can be formulated.

Summary of the Invention

Large gene families encoding mammalian olfactory G-protein-coupled receptors (OLFR) and mammalian taste G-protein-coupled receptors (TASR) are known in the prior art or are disclosed herein. An object of the invention to provide fragments and variants of such OLFRs and TASRs which retain odorant- or tastant-binding activity, respectively. The large number of sensory receptors that are made available herein and now amendable to manipulation raises the confidence that a substantially complete, or at least functional, repertoire of sensory receptors is provided.

It is an object of the invention to provide nucleic acid sequences or molecules that encode such sensory receptors, or fragments or variants thereof. Another object is to provide expression vectors which include nucleic acid sequences that encode such sensory receptors, or fragments or variants thereof. It is yet another object of the invention to provide human or non-human cells which functionally express at least one of such sensory receptors, or fragments or variants thereof. Still another object is to provide sensory receptor fusion proteins or other polypeptides which include at least a fragment of at least one of such sensory receptors. In particular, fusions with reporter molecules or other heterologous amino acid sequences may maintain the original ligand-properties while changing the signaling properties to allow easier detection of sensant binding to the receptor (*e.g.*, change in fluorescent signal). Moreover, chimeric proteins or other polypeptides with altered ligand-binding and/or signaling properties can be made from two or more different sensory receptors by mixing domains.

The invention provides methods for representing the sensory perception of one or more chemicals (*e.g.*, a primary sensant or mixture thereof) and/or for predicting the sensory perception of one or more chemicals in a mammal (*e.g.*, human) using the aforementioned products. Given a known member of a ligand-receptor binding pair, one or both members of the pair (*i.e.*, ligand, receptor, or both) may be detected, identified, and/or measured under binding conditions.

Novel molecules or combinations of molecules which elicit a desired and predetermined sensory perception in a mammal (*e.g.*, human) can be generated by determining a value of sensory perception in a mammal for a known molecule or combination thereof; determining a value of sensory perception in a mammal for one or more unknown molecules or combinations thereof; comparing the value of sensory perception in a mammal for one or more unknown compositions to the value of sensory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined sensory perception in a mammal; and mixing two or more unknown molecules or combinations thereof to form a molecule or combination thereof that elicits a predetermined sensory perception in a mammal. The combining step yields a single molecule or a combination thereof that elicits a predetermined sensory perception in a mammal. In particular, primary odorants that uniquely bind to olfactory receptors with a single

ligand-binding domain may be such novel molecules. Variants thereof may be used (1) to enhance stimulation of a limited response by olfactory receptors with a single ligand-binding domain or (2) to block stimulation of olfactory receptors with a single ligand-binding domain to reduce or inhibit olfactory perception. An alternative method for identifying primary odorants is to identify the mutated receptors in genetic anosmias because that odorant would be expected to be recognized by only one or a few olfactory receptors affected by the mutation.

Detailed Description of the Invention

10 Perception of Chemical Sensants

U.S. Patent No. 5,691,188 describes how upon binding of ligand to receptor, the receptor presumably undergoes a conformational change leading to activation of the G protein. The G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of disso-ciation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell. A high-resolution X-ray crystal structure is available for rhodopsin, a guanyl nucleotide binding protein, has been solved (Palczewski *et al.*, *Science* 289:739, 2000). Using this structure, the portions of the amino acid sequence of sensant receptors that are responsible for ligand binding can be identified.

30

Sensory Perception - Olfaction

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel *Sci. Amer.* 273:154, 1995). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer *Semin. Cell Biol.* 5:25, 1994). The human genome contains thousands of genes that encode a diverse repertoire of olfactory receptors (Rouquier *Nat. Genet.* 18:243, 1998; Trask *Hum. Mol. Genet.* 7:2007, 1998). An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that sensory receptors belong to a multigene family with over a thousand members, and the odorant receptors number at least 500 to 1,000. Moreover, each sensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses.

Sensory Perception - Taste

Mammals are believed to have five basic taste modalities: sweet, bitter, sour, salty, and umami (the taste of monosodium glutamate). See, e.g., Kawamura *et al.*, *Introduction to Umami: A Basic Taste* (1987); Kinnamon *et al.*, *Ann. Rev. Physiol.*, 54:715, 1992; Lindemann, *Physiol. Rev.*, 76:718, 1996; Stewart *et al.*, *Am. J. Physiol.*, 272:1, 1997. Numerous physiological studies in animals have shown that taste receptor cells may selectively respond to different chemical stimuli. See, e.g., Akabas *et al.*, *Science*, 242:1047, 1988; Gilbertson *et al.*, *J. Gen. Physiol.*, 100:803, 1992; Bernhardt *et al.*, *J. Physiol.*, 490:325, 1996; Cummings *et al.*, *J. Neurophysiol.*, 75:1256, 1996.

In mammals, taste receptor cells are assembled into taste buds that are distributed into different papillae in the tongue epithelium. Circumvallate papillae, found at the very back of the tongue, contain hundreds, e.g., mice, to thousands, e.g., human, of taste buds. By contrast, foliate papillae, localized to the posterior lateral edge of the tongue, only contain dozens to hundreds of taste buds. Moreover, fungiform papillae contain only a single or a few taste buds, and are at the front of the tongue.

Each taste bud, depending on the species, contains 50-150 cells, including precursor cells, support cells, and taste receptor cells. *See, e.g., Lindemann, Physiol. Rev.*, 76:718, 1996. Receptor cells are innervated at their base by afferent nerve endings that transmit information to the taste centers of the cortex through synapses in the brain stem and thalamus. Elucidating the mechanisms of taste cell signaling and information processing is critical for understanding the function, regulation, and perception of the sense of taste.

Exemplary bitter substance are of 6-n-propylthiouracil (PROP), sucrose octaacetate (soa), raffinose undecaacetate (rua), cycloheximide (cyx), denatonium, copper glycinate (GI), and quinine (qui), which bind one or more T2R taste receptors.

Structure of Receptors for Chemical Sensants

Complete or partial sequences of numerous human and other eukaryotic sensory receptors are currently known. *See, e.g., Pipel et al., Protein Sci.*, 8:969, 1999; Mombaerts, *Annu. Rev. Neurosci.*, 22:487, 1999. *See also*, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282.

Genes encoding two hundred fifty-six (256) distinct, novel human olfactory receptors have been identified in genome sequence databases. All of the receptor genes have been initially detected by a computer DNA sequence analysis in the corresponding partially sequenced human BAC genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986,

- AC010814, AC018700, AC021304, AC008620, AC011537, AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654,
- 5 AP001803, AP001804, AL353767, AP001884, AC026083, AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365,
- 10 AP002826, AL359636, AL391534, AC055731, AC076959, AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes. Similarly, genes encoding five and thirty-six (36) distinct, novel human T1R and T2R taste receptors, respectively, have been identified in genome
- 15 sequence databases.

Alternatively, nucleic acids encoding the sensory receptors and other related polypeptides can be isolated from a variety of sources, genetically engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 00/35374, which is herein incorporated by reference in its entirety.

- 20 These nucleic acids provide probes for the identification of cells expressing sensory receptors, as the nucleic acids are specifically expressed in such cells. They can also serve as tools for the generation of sensory topographical maps that elucidate the relationship between cells expressing sensory receptors and sensory neurons leading to particular regions of the brain. Furthermore, the nucleic acids and the
- 25 polypeptides they encode can be used as probes to elucidate olfactant- or tastant-induced behaviors.

- Nucleic acid molecules encoding a sensory receptor comprising a nucleic acid sequence that is at least 75%, 85%, 90%, 95%, or 99% identical to a nucleic acid sequence selected from those known in the prior art or disclosed herein are considered
- 30 variants. Other nucleic acid molecules comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence at least 75%, 85%, 90%, 95%, or 99% identical to an amino acid sequence selected from those known in the prior art or disclosed herein are also considered variants. Further variants contain amino acid

sequence differences in at most ten, five, four, three, two, or one amino acid residue(s).

Exemplary nucleic acid sequences may be selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, 5 SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, 10 SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, 15 SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, 20 SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, 25 SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, 30 SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID

NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288,
SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID
NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306,
SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID
5 NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324,
SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID
NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342,
SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID
NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360,
10 SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID
NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378,
SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID
NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396,
SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID
15 NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414,
SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID
NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432,
SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID
NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450,
20 SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID
NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468,
SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID
NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486,
SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID
25 NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504,
SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512.

Nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from those known in the prior art or disclosed herein; wherein the fragment is at least ten, 20, 30, 50, 70, 100, or 150 amino acid residues in length, are useful as probes, primers, and to construct hybrids or chimerae.

Polypeptides comprising an amino acid sequence that is at least 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from those

known in the prior art or disclosed herein are considered variants. Further variants contain amino acid sequence differences in at most ten, five, four, three, two, or one amino acid residue(s). Other polypeptides comprising a fragment of a polypeptide having an amino acid sequence selected from those known in the prior art or disclosed herein; wherein the fragment is at least 40, 60, 80, 100, 150, 200, or 250 amino acid residues in length, are useful as specific binders of sensants, competitive binders, antigens, and to construct hybrids or chimeras.

Exemplary amino acid sequences may be selected from the group consisting of

SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,

SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID
 NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253,
 SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID
 NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271,
 5 SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID
 NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,
 SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID
 NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307,
 SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID
 10 NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,
 SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID
 NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,
 SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID
 NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361,
 15 SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID
 NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,
 SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID
 NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,
 SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID
 20 NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,
 SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID
 NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,
 SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID
 NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,
 25 SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
 NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
 SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
 NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
 SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID
 30 NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
 SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Also provided are methods of screening for modulators, *e.g.*, activators, inhibitors, stimu-lators, enhancers, agonists, and antagonists, of the sensory receptors.

or fragments or variants thereof. Such modulators of signal transduction are useful for pharmacological or genetic modulation of signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of sensory cell activity. These modulator compounds can then be used in the pharmaceutical, food, and cosmetic industries to customize odorants or tastants.

Thus, the invention provides assays for sensory modulation, where the sensory receptors, or fragments or variants thereof, act as direct or indirect reporter molecules for the effect of modulators on signal transduction. Sensory receptors, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo*, and *ex vivo*. In one embodiment, sensory receptors, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g., Mistili et al., Nature Biotech.*, 15:961, 1997). In another embodiment, the sensory receptors, or fragments or variants thereof, can be expressed in host cells, and modulation of signal transduction via sensory receptor activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of signal transduction include *in vitro* ligand binding assays using the sensory receptors, or fragments or variants thereof. More particularly, such assays can use the sensory receptors; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G-protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting sensory receptor nucleic acid and protein expression, allowing for the investigation of taste transduction regulation and specific identification of sensory receptor cells. The sensory receptors, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying a sensory receptor cells. Sensory receptor cells can be identified using techniques such as reverse transcription and amplification

of mRNA, isolation of total RNA or poly A⁺ RNA, Northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, Western blots, and the like.

A. Identification and Characterization of Sensory Receptors

- 5 The amino acid sequences of the sensory receptors and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.
- 10 For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as
- 15 described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

- 20 A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment
- 25 of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443, 1970, by the search for similarity method of Pearson & Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and
- 30 TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J. Mol. Biol.* 215:403, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nucl. Acids Res.* 25:3389, 1977 and Altschul *et al.*, *J. Mol. Biol.* 215:403, 1990). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive

alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351, 1987. The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151, 1989. The program can align up to 300 sequences, each of a maximum length of 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the

5 pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by

10 designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can

15 be obtained from the GCG sequence analysis software package, *e.g.*, version 7.0 (Devereaux *et al.*, *Nucl. Acids Res.* 12:387, 1984) encoded by the genes were derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian

20 olfactory receptor family, each of the olfactory receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative sensory receptor proteins generally having lengths of about 300 to

25 about 400 amino acid residues that contain seven transmembrane domains, as predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the 256 sensory receptors identified herein has a characteristic sequence signature of an olfactory

30 receptor. In particular, all 256 sequences contain very close matches to the following consensus amino acid motifs (Mombaerts, 1999; Pilpel, 1999): LHTPMY in intracellular loop 1, MAYDRYVAIC at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5,

FSTCSSH in the beginning of transmembrane domain 6, and PMLNPF in transmembrane domain 7. Combination of all the above mentioned structural features of the 256 genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

As noted above, complete or partial sequences of numerous human and other eukaryotic sensory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human sensory receptors, which suggests their different specificity in sensant recognition. Therefore, these novel sensory receptors and their genes can be used, alone or in combination with known sensory receptors, in developing detection systems and assays for chemically distinct types of sensants not recognized by the known sensory receptors, as well as for diagnostic and research purposes.

B. Definitions

The terms "purified," "substantially purified," and "isolated" as used herein refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

00000000-00000000

The terms “amplifying” and “amplification” refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, sensant-binding sequences of the invention) *in vivo* or *in vitro*.

The term “7- transmembrane receptor” means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma membrane seven times (thus, the seven domains are called “transmembrane” or “TM” domains TM I to TM VII). The families of olfactory and taste receptors each belong to this super-family. Seven-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

The term “expression vector” refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, *i.e.*, drive only transient expression in a cell. The term includes recombinant expression “cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

The term “library” means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated sensory, particularly olfactory or taste, receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of vectors that incorporate the amplified sensant-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding a sensory receptor.

The term “nucleic acid” or “nucleic acid sequence” refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, *i.e.*, oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like

structures with synthetic backbones, see e.g., *Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Anti-sense Strategies*, Annals of the N.Y. Academy of Sciences, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan (1993) *J. Med. Chem.* 36:1923-1937; *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata (1997) *Toxicol. Appl. Pharmacol.* 144:189-197; Strauss-Soukup (1997) *Biochemistry* 36:8692-8698; Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156.

The term sensory receptor "ligand-binding region" refers to sequences derived from a sensory receptor that substantially incorporates transmembrane domains II to VII (TM II to VII). The domain may be capable of binding a sensant.

The terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the poly-peptide's (the conservative variant's) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, i.e., amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (e.g., acidic, basic, positively or negatively charged, polar or non-polar, etc.) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing function-ally similar amino acids are well known in the art.

For example, one exemplary guideline to select conservative substitutions includes (original residue followed by exemplary substitution): Ala/Gly or Ser; Arg/Lys; Asn/Gln or His; Asp/Glu; Cys/Ser; Gln/Asn; Gly/Asp; Gly/Ala or Pro; His/Asn or Gln; Ile/Leu or Val; Leu/Ile or val; Lys/Arg or Gln or Glu; Met/Leu or Tyr or Ile; Phe/Met or Leu or Tyr; Ser/Thr; Thr/Ser; Trp/Tyr; Tyr/Trp or Phe; Val/Ile or Leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (see also, e.g., Creighton, *Proteins*, W.H. Freeman, 1984; Schultz & Schimer, *Principles of Protein Structure*, Springer-Verlag, 1979). One of skill in the art will appreciate that the above-identified substitutions are not the only possible

conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered “conservatively modified variations.”

The terms “mimetic” and “peptidomimetic” refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains or sensant-binding domains or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic’s structure and/or activity. As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups:

- a) residue linkage groups other than the natural amide bond (“peptide bond”) linkages;
- b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds.

Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N’-dicyclohexylcarbodiimide (DCC) or N,N’-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond (“peptide bond”) linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (see, *e.g.*, Spatola (1983) in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, “Peptide Backbone Modifications,”

Marcell Dekker, NY). A polypeptide can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (e.g., "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, e.g., inducible or constitutive expression of a fusion protein comprising a translocation domain of the invention and a nucleic acid sequence amplified using a primer of the invention.

The term "transmembrane domain" means a polypeptide domain that can completely span the plasma membrane. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below.

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the sensory receptors, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (e.g., promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, e.g., bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, e.g., Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature. See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I, Theory and Nucleic Acid Preparation*, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assay (ELISA), immunofluorescent assay, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-PAGE),

RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (*PCR Protocols, a Guide to Methods and Applications*, ed. Innis. Academic Press, NY, 1990 and *PCR Strategies*, ed. Innis, Academic Press, NY, 1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560, 1989; Landegren, *Science* 241:1077, 1988; Barringer, *Gene* 89:117, 1990); transcription amplification (see, e.g., Kwok, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989); and, self-sustained sequence replication (see, e.g., Guatelli, *Proc. Natl. Acad. Sci. USA* 87:1874, 1990); Q Beta replicase amplification (see, e.g., Smith, *J. Clin. Microbiol.* 35:1477, 1997); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257, 1996) and other RNA polymerase mediated techniques (e.g., NASBA, Cingene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307, 1987; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563, 1995.

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, e.g., U.S. Patent No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the sensant-binding region-coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted sensant-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I

and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (e.g., hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (e.g., do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify sensant-binding regions of olfactory receptor proteins. These domain regions may vary for different sensnants, and more particularly odorants; thus, what may be a minimal binding region for one sensant, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (e.g., only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane sensory receptor.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII.

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3'). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify a transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL_n, encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CA-NGT-3'. Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (see, e.g., Rose, *Nucl. Acids Res.* 26:1628, 1998; Singh, *Biotechniques* 24:318, 1998).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. See, e.g., Hoops, *Nucleic Acids Res.* 25:4866, 1997. Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (see, e.g., Morales, *Nat. Struct. Biol.* 5:950, 1998). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (see, e.g., Hill, *Proc. Natl. Acad. Sci. USA* 95:4258, 1998). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, see above). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' and 5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' and 5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' and 5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3'.

Nucleic acids that encode ligand-binding regions of olfactory receptors are generated by amplification (*e.g.*, PCR) of appropriate nucleic acid sequences using degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova, *Proc. Natl. Acad. Sci. USA* 93:9858, 1996). Shirley, *Eur. J. Biochem.* 32:485, 1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211, 1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*,

antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260, 1999), describes differentiated olfactory receptor-expressing cells in culture that respond to odorants, as measured by an influx of calcium.

5 Hybrid protein-coding sequences comprising nucleic acids sensory receptors fused to the translocation sequences described herein may be constructed. Also provided are hybrid receptors comprising the translocation motifs and ligand-binding domains of sensory receptors. These nucleic acid sequences can be operably linked to transcriptional or translational control elements, e.g., transcription and translation
10 initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can
15 also be used to express the fusion polypeptide receptor, including, e.g., a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227, 1998). Receptor genes are normally expressed in a small subset of
20 neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

Fusion proteins, either having C-terminal or, more preferably, N-terminal
25 translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional elements for, e.g., protein detection, purification, or other applications. Detection and purification facilitating domains include, e.g., metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized
30 metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289, 1998), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615, 1997); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a nucleic acid sequence encoding a polypeptide linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787, 1995), and an amino terminal translocation domain. The histidine residues facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, *see, e.g., Kroll, DNA Cell. Biol.* 12:441, 1993).

Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent literature. *See, e.g., Roberts, Nature* 328:731, 1987; Berger *supra*; Schneider, *Protein Expr. Purif.* 6:435:10, 1995; Sambrook; Tijssen; Ausubel. Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g., episomal expression systems*). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g., chloramphenicol, kanamycin, G418, bleomycin, hygromycin*) or herbicide resistance (*e.g., chlorosulfuron or Basta*) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g., Blondelet-Rouault, Gene* 190:315, 1997; Aubrecht, *J. Pharmacol. Exp. Ther.* 281:992, 1997). Because

selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a sensant-binding domain within any 7-transmembrane polypeptide. Seven-transmembrane receptors belong to a superfamily of trans-membrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-trans-membrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (e.g., TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969, 1999; Rost, *Protein Sci.* 4:521, 1995. Periodicity detection enhancement and alpha helical periodicity index can be done as by, e.g., Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.,* Peitsch, *Receptors Channels* 4:161, 1996; Cronet, *Protein Eng.* 6:59, (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, e.g., TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (e.g., PCR) from mRNA of or cDNA derived from, e.g., olfactory receptor-expressing neurons or genomic DNA.

Libraries of sensory receptor ligand-binding TM domain sequences can include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, e.g., homology modeling, Fourier analysis and helical periodicity (*see, e.g.,* Pilpel *supra*), as described above. Using this information sequences flanking the seven

domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,
5 for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the sensory receptors described herein, coupled to additional amino acids representing all or part of another
10 G protein receptor, preferably a member of the 7-transmembrane superfamily. These chimerae can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the 7-transmembrane protein described herein, and the
15 remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled in the art can readily be used to create such chimeric receptors. The use of such
20 chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand binding domain, an extracellular
25 domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous CGPCR
30 extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, e.g., green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to a sensory receptor disclosed herein can be isolated using the nucleic acid probes described above. Alternatively, expression libraries can be used to isolate sensory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against a sensory receptor-derived polypeptide, which also recognize and selectively bind to the sensory receptor homolog.

Also within the scope of the invention are host cells for expressing the sensory receptors, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the sensory receptors, fragments, or variants thereof, the nucleic acid sequence of interest is subcloned into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable prokaryotic and eukaryotic expression systems are well known in the art and described, e.g., in Sambrook *et al.*

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasmid vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.,* Sambrook *et al.*). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.,* WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of Sensory Receptor Polypeptides

In addition to the detection of sensory receptor genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect

sensory receptors, e.g., to identify olfactory receptor cells, and variants of sensory receptor family members. Immunoassays can be used to qualitatively or quantitatively analyze the sensory receptors. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

5 1. Antibodies to sensory receptor family members

 Methods of producing polyclonal and monoclonal antibodies that react specifically with a sensory receptor family member are known to those of skill in the art (see, e.g., Coligan, *Current Protocols in Immunology*, 1991; Goding, *Monoclonal Antibodies: Principles and Practice*, 2d ed., 1986; Harlow & Lane, supra; and Kohler & Milstein, *Nature*, 256:495, 1975). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (see, e.g., Huse et al., *Science*, 246:1275, 1989; Ward et al., *Nature*, 341:544, 1989).

15 A number of sensory receptor-comprising immunogens may be used to produce antibody specifically reactive with a sensory receptor family member. For example, a recombinant sensory receptor protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, e.g., the conserved motifs that are used to identify members of the sensory receptor family.

20 Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Naturally occurring

25 protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

 Methods of production of polyclonal antibodies are known to those of skill in the art. Mice, hamsters, rats, guinea pigs, rabbits, goats, or chickens is immunized with the protein using an adjuvant (e.g., Freund's adjuvant) and a standard immunization protocol with periodic boosts. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of

reactivity to the sensory receptor. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (see Harlow & Lane, *supra*).

5 Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (see Kohler & Milstein, *Eur. J. Immunol.*, 6:511, 1976). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, retroviruses, or other
10 methods well known in the art. Colonies arising from single clones of immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a
15 monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275, 1989.

 Monoclonal antibodies or polyclonal sera are collected and titered against antigen in an immunoassay, for example, a solid phase immunoassay with the antigen
20 immobilized on a solid support. Typically, polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against non-sensory receptor proteins, or even other sensory receptor family members or other related proteins from other organisms, using a competitive binding immuno-assay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a Kd of at least about 0.1
25 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

 Once sensory receptor family member specific antibodies are available, individual sensory receptor proteins can be detected by a variety of immunoassay methods. For a review of immuno-nological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed., 1991). Moreover, the
30 immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

2. Immunological binding assays

Sensory receptor proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patent Nos. 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general

5 immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed., 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case a sensory receptor family member or an antigenic subsequence thereof). The antibody (e.g., anti-sensory
10 receptor) may be produced by any of a number of means well known to those of skill in the art and as described above.

Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent
15 may be a labeled sensory receptor polypeptide or a labeled anti-sensory receptor antibody. Alternatively, the labeling agent may be a third moiety, such as a secondary antibody, that specifically binds to the antibody/sensory receptor complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding
20 immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (see, e.g., Kronval *et al.*, *J. Immunol.*, 111:1401, 1973; Akerstrom *et al.*, *J. Immunol.*, 135:2589, 1985). The labeling agent can be modified with a detectable moiety, such as biotin, to which
25 another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the
30 incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting a sensory receptor protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays directly measure the amount of antigen. In one preferred “sandwich” assay, for example, the
5 anti-sensory receptor antibodies are bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the sensory receptor protein present in the test sample. The sensory receptor protein thus immobilized is then bound by a labeling agent, such as a second anti-sensory receptor antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in
10 turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g.*, streptavidin, to provide a detectable moiety.

b. Competitive assay formats

15 In competitive assays, the amount of sensory receptor protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) sensory receptor protein displaced (competed away) from an anti-sensory receptor antibody by the unknown sensory receptor protein present in a sample. In one competitive assay, a known amount of sensory receptor protein is added to a
20 sample and the sample is then contacted with an antibody that specifically binds to the sensory receptor. The amount of exogenous sensory receptor protein bound to the antibody is inversely proportional to the concentration of sensory receptor protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of sensory receptor protein bound to
25 the antibody may be determined either by measuring the amount of sensory receptor protein present in a sensory receptor/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of sensory receptor protein may be detected by providing a labeled sensory receptor molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay
30 the known sensory receptor protein is immobilized on a solid substrate. A known amount of anti-sensory receptor antibody is added to the sample, and the sample is then contacted with the immobilized sensory receptor. The amount of anti-sensory receptor antibody bound to the known immobilized sensory receptor protein is

inversely proportional to the amount of sensory receptor protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, sensory receptor proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the sensory receptor polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percentage cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the sensory receptor family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a sensory receptor family member, to the immunogen protein (*i.e.*, sensory receptor protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to

specifically bind to the polyclonal antibodies generated to a sensory receptor immunogen.

Antibodies raised against sensory receptor conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the sensory receptor family, but not to GPCRs from other families. Polyclonal antibodies that specifically bind to a particular member of the sensory receptor family, can be made by subtracting out cross-reactive antibodies using other sensory receptor family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human T2R01 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OLFR1 or mouse OLFR1.

d. Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of sensory receptor protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the sensory receptor protein. The anti-sensory receptor polypeptide antibodies specifically bind to the sensory receptor poly-peptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-sensory receptor antibodies.

Other assay formats include liposome immunoassays (LIA) using liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34, 1986).

e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein

compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f. Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immuno-assays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, bio-chemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS™, fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C, or ³²P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, etc.).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to another molecules (e.g., streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a sensory receptor protein, or secondary antibodies that recognize anti-sensory receptor.

The molecules can also be conjugated directly to signal generating compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone,

etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, e.g., luminol. For a review of various labeling or signal producing systems that may be used, see U.S. Patent No. 4,391,904.

Methods for detecting labels are well known. Thus, for example, where the label is a radioactive label, it may be detected using a scintillation counter or with photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluoro-chrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, with photographic film, or using electronic detectors such as charge coupled devices (CCDs) or photomultipliers. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian sensory, and more particularly, olfactory receptor of the invention, both *in vitro* and *in vivo* are described below, as are methods and compositions for determining whether a test compound is neurotoxic to an olfactory neuron expressing an olfactory transmembrane receptor polypeptide. Any aspect of cell physiology can be monitored to assess the effect of sensant-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical

stimuli into electrical signals. An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G-proteins, and modulation of diverse channels by Gi and other G-proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The sensory receptor protein of the assay will typically be selected from a natural poly-peptide or conservatively modified variant thereof. Generally, the amino acid sequence identity will be at least 75%, 85%, 90%, 95%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of a sensory receptor protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand binding domain, subunit association domain, active site, and the like. Either the sensory receptor protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein.

Modulators of sensory receptor activity can be tested using sensory receptor polypeptides as described above, either recombinant or naturally occurring. Protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. In vitro binding assays

Sensory perception can also be examined *in vitro* with soluble or solid state reactions, using a full-length sensory receptor-GPCR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a sensory receptor covalently linked to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of a sensory receptor. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises all or part of a sensory receptor polypeptide, as well an additional sequence that facilitates the localization of the

0000055.052201
sensory receptor to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein.

Ligand binding to a sensory receptor protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties. Sensory receptors with large (*e.g.*, approximately 600 amino acid residues) extracellular N-terminal segments. These N-terminal segments are thought to form ligand-binding domains, and are therefore useful in biochemical assays to identify sensory receptor agonists and antagonists. Similar assays have been used with other GPCRs, such as the metabo-tropic glutamate receptors (*e.g.*, Han & Hampson, *J. Biol. Chem.* 274:10008, 1999). These assays might involve displacing a radioactively or fluorescently labeled ligand, and measuring changes in intrinsic fluorescence or changes in proteolytic susceptibility, *etc.*

Receptor-G-protein interactions can also be examined. For example, binding of the G-protein to the receptor or its release from the receptor can be examined. For example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G-protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G-protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor sensant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation, or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the sensory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nano-seconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the sensory receptors of the invention, fluorescence-labeled sensants or auto-fluorescent sensants may be used. Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and \perp is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For

example, the Beacon® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley *J. Anal. Toxicol.* 5, 236, 1981 which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$\text{Rotational Relaxation Time} = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (≈ 1 nanosecond) for small molecules (e.g., fluorescein) and large (≈ 100 nanoseconds) for large molecules (e.g., immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Soluble and solid state high throughput assays

In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand binding domain, an extracellular domain, a transmembrane domain (e.g., one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous protein to create a chimeric molecule; a sensory receptor protein; or a cell or tissue expressing a sensory receptor protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the domain, chimeric molecule, sensory receptor protein, or cell or tissue expressing the sensory receptor is attached to a solid phase substrate.

In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (e.g., 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, e.g., via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (e.g., the taste transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, etc.). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (see, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (e.g., cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,

immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; see, e.g., Pigott & Power, *The Adhesion Molecule Facts Book I* 1993). Similarly, toxins and venoms, viral epitopes, hormones (e.g., opiates, steroids, etc.), intracellular receptors (e.g., which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, poly-amides, polyethyleneimines, polyarylene sulfides, polysiloxanes, polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethyne glycol) linkers are available from Shearwater Polymers (Huntsville, AL). The linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent which fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups which are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Amino-alkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. See, e.g., Merrifield, *J. Am. Chem. Soc.* 85:2149, 1963 (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.* 102:259, 1987 (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron* 44:6031, 1988 (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science* 251:767, 1991; Sheldon *et al.*, *Clinical Chemistry* 39:718, 1993; and Kozal *et al.*, *Nature Medicine*, 2:753, 1996 (all

describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

5 Yet another assay for compounds that modulate sensory receptor protein activity involves computer assisted drug design, in which a digital or analog processing system is used to generate a three-dimensional structure of a sensory receptor protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a
10 preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, *e.g.*, ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering
15 protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a sensory receptor polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of those described herein, or fragments or variants thereof.

20 The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*,
25 magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.

30 The amino acid sequence represents a primary structure that encodes the information necessary to form the secondary, tertiary and quaternary structure of the protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent

accessible surfaces, and hydrogen bonding. Secondary energy terms include van der Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the sensory receptor protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of sensory receptor genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used to identify patients having such mutated genes. Identification of the mutated sensory receptor genes involves receiving input of a first nucleic acid or amino acid sequence of a sensory receptor gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once

the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified. Such sequences can represent allelic differences in various sensory receptor genes, and mutations associated with disease states and genetic traits.

5 5. Cell-based binding assays

In a preferred embodiment, a sensory receptor polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an
10 N-terminal fragment of a rhodopsin. Such chimeric sensory receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, Gal 5, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected
15 using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of ³²P from gamma-labeled GTP to the receptor, which can
20 be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G-proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired
25 odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, see, *e.g.*, *Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

30 Samples or assays that are treated with a potential sensory receptor protein inhibitor or activator are compared to control samples without the test compound, to examine the extent of modulation. Such assays may be carried out in the presence of an odorant that is known to activate the particular receptor, and modulation of the

odorant dependent activation monitored. Control samples (untreated with activators or inhibitors) are assigned a relative sensory receptor activity value of 100. Inhibition of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of a sensory receptor protein is achieved when the sensory receptor activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a sensory receptor protein. One means to determine changes in cellular polarization is by measuring changes in current, and thereby measuring changes in polarization, with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575, 1997). Whole cell currents are conveniently determined using the standard. Other known assays include: assays to measure ion flux using radiolabeled or fluorescent probes such as voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67, 1988; Gonzales & Tsien, *Chem. Biol.*, 4:269, 1997; Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185, 1991; Holevinsky *et al.*, *J. Membrane Biology*, 137:59, 1994). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, Northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP₃, cGMP, or cAMP.

Preferred assays for G-protein coupled receptors include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G-protein coupled receptors as negative or positive controls to assess activity of tested compounds. In assays for identifying modulatory compounds (*e.g.*, agonists,

antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed in the Molecular Probes 1997 Catalog. For G-protein coupled receptors, promiscuous G-proteins such as $G\alpha 15$ and $G\alpha 16$ can be used in the assay of choice (Wilkie *et al.*, *Proc. Natl. Acad. Sci.*, 88:10049, 1991). Such promiscuous G-proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*, increases in second messengers such as IP₃, which releases intracellular stores of calcium ions. Activation of some G-protein coupled receptors stimulates the formation of inositol triphosphate (IP₃) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature* 312:315, 1984). IP₃ in turn stimulates the release of intracellular calcium ion stores. Thus, a change in cytoplasmic calcium ion levels, or a change in second messenger levels such as IP₃ can be used to assess G-protein coupled receptor function. Cells expressing such G-protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (see, *e.g.*, Altenhofen *et al.*, *Proc. Natl. Acad. Sci.*, 88:9868, 1991 and Dhallan *et al.*, *Nature* 347:184, 1990). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*, certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors,

serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, sensory receptor protein activity is measured by expressing a sensory receptor gene in a heterologous cell with a promiscuous

- 5 G-protein that links the receptor to a phospholipase C signal transduction pathway (see Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995). Optionally the cell line is HEK-293 (which does not naturally express sensory receptor genes) and the promiscuous G-protein is Gal 5 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by measuring changes in intracellular Ca^{2+} levels, 10 which change in response to modulation of the sensory receptor signal transduction pathway via administration of a molecule that associates with a sensory receptor protein. Changes in Ca^{2+} levels are optionally measured using fluorescent Ca^{2+} indicator dyes and fluorometric imaging.

- In one embodiment, the changes in intracellular cAMP or cGMP can be 15 measured using immunoassays. The method described in Offermanns & Simon, *J. Biol. Chem.*, 270:15175, 1995, may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159, 1994, may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent No. 4,115,538, herein 20 incorporated by reference.

- In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent No. 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and 25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the presence of buffer control (which may or may not contain an agonist). 30

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing a sensory receptor protein of interest is contacted with a test compound for a sufficient time to

effect any interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent No. 5,436,128, herein incorporated by reference. The reporter genes can be, e.g., chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (see, e.g., Mistili & Spector, *Nature Biotech.* 15:961, 1997).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the sensory receptor protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the sensory receptor protein of interest.

6. Transgenic non-human animals expressing sensory receptors

Non-human animals expressing one or more sensory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of translocation domains in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize

odorants/ligands that can bind to a specific or sets of receptors. Such vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

- 5 Means to infect/express the nucleic acids and vectors, either individually or as libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses.
- 10 When electrodes are located on the olfactory bulb surface it is possible to record stable responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287, 1997). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of
- 15 one turbinate bone or were placed in corresponding positions on four turbinate bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950, 1997; Scott, *J. Neurophysiol.* 75:2036, 1996; Ezech, *J. Neurophysiol.* 73:2207, 1995. In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and
- 20 medial surface of the turbinates (*see, e.g.*, Youngentob, *J. Neurophysiol.* 73:387, 1995). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1, 1991).

- 25 The sensory receptor sequences of the invention can be for example expressed in animal nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *Proc. Natl. Acad. Sci. USA* 96:4040, 1999.

- 30 The endogenous olfactory receptor genes can remain functional and wild-type (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a “knockout” cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or
5 completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, “gene trap insertion” can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97, 1997). The insertion of the exogenous is typically by
10 homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene’s expression; or a combination thereof. Gene targeting via homologous recombination in pluripotential embryonic stem (ES) cells
15 allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53, 1998); Moreadith, *J. Mol. Med.* 75:208, 1997; Tojo, *Cytotechnology* 19:161, 1995; Mudgett, *Methods Mol. Biol.* 48:167, 1995; Longo, *Transgenic Res.* 6:321, 1997; U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992;
20 5,627,059; 5,272,071; WO 91/09955; WO93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries can also be used as reagents to produce “knockout” human cells and their progeny.

F. Modulators

25 The compounds tested as modulators of a sensory receptor family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of a sensory receptor gene. Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential
30 modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by

automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO),

5 Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such

10 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

15 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a

20 given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not

25 limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka, *Int. J. Pept. Prot. Res.* 37:487, 1991; and Houghton *et al.*, *Nature* 354:84, 1991). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (e.g., WO 91/19735), encoded peptides (e.g., WO 93/20242), random bio-oligomers (e.g., WO 92/00091),

30 benzodiazepines (e.g., U.S. Patent No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci.* 90:6909, 1993), vinyllogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568, 1992), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer.*

- Chem. Soc.* 114:9217, 1992), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661, 1994), oligo-carbamates (Cho *et al.*, *Science* 261:1303, 1993), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658, 1994), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*),
- 5 peptide nucleic acid libraries (U.S. Patent No. 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology* 14:309, 1996 and WO 97/00271), carbohydrate libraries (Liang *et al.*, *Science* 274:1520, 1996) and U.S. Patent No. 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, page 33, Jan 18, 1993); thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pynrolidines, U.S.
- 10 Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514, and the like.

- Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville, KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA),
- 15 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

G. Methods for Representing and Predicting Sensant Perception

- 20 The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal (*e.g.*, human). Preferably, such methods may be performed by using the receptors and genes encoding the sensory receptors disclosed herein, or fragments or variants thereof.

- 25 Also provided is a method of screening a chemical sample for the presence of an odor or taste sensed by a mammal (*e.g.*, human), comprising: contacting the chemical sample with one or more of the aforementioned products and detecting binding between sensant ligand and sensory receptor. The sensory receptor, or fragments or variants thereof (*e.g.*, fusion proteins with repor-ters, chimeric proteins)
- 30 may be expressed in cells; otherwise, ligand-binding domain(s) may be fixed to a substrate (*e.g.*, substantially planar, bead, or fiber) that is solid or porous. The product used in this method is considered a biosensor.

Moreover, a method is provided for simulating a fragrance or flavor sensed by a mammal (e.g., human), comprising: for each of a plurality of sensory receptors, or fragments or variants thereof, ascertaining the extent to which the sensory receptor interacts with the fragrance and/or flavor; and combining a plurality of compounds, each having a previously-determined interaction with one or more of the sensory receptors, in amounts that together provide a stimulation profile that mimics the profile for the fragrance and/or flavor. Interaction of a fragrance and/or flavor with a sensory receptor can be determined using any of the binding or reporter assays described herein. The interactions can be aggregated or a profile generated using known signal processing techniques (e.g., a neural network) as described below. The sensory receptor, or fragments or variants thereof (e.g., fusion proteins with reporters, chimeric proteins) may be expressed in cells; otherwise, ligand-binding domain(s) may be fixed to a substrate (e.g., planar, bead, or fiber) that is solid or porous. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80%, 90%, 95%, 99% or all of the receptors that are substantially stimulated by the fragrance or flavor.

In yet another aspect of the invention, a method is provided in which a plurality of standard compounds are tested against a plurality of sensory receptors, or fragments or variants thereof, to ascertain the extent to which the sensory receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on data storage medium. The method may further comprise providing a desired receptor-stimulation profile for an odor and/or taste; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the odor and/or taste.

A further aspect of the invention is to provide a method for representing sensory perception of a particular odor and/or taste in a mammal (e.g., human), comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is

greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; and generating from the values a quantitative representation of sensory perception. The sensory receptors may be a receptor disclosed herein, or fragments or variants thereof. The representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, or may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced sensory receptors, or fragments or variants thereof, with a composition and quantitatively measuring the interaction of the composition with the receptors. The maximum number of taste receptors that are needed to mimic the native repertoire (e.g., about 50) may be less than the maximum number of olfactory receptors that are needed (e.g., about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

It is yet another aspect of the invention to provide a method for predicting the sensory perception in a mammal (e.g., human) generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in the mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding known sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n sensory receptors of the mammal; where n is

greater than or equal to 5, n is greater than or equal to 10, n is greater than or equal to 20, n is greater than or equal to 50, n is greater than or equal to 75, n is greater than or equal to 100, n is greater than or equal to 125, n is greater than or equal to 150, n is greater than or equal to 175, n is greater than or equal to 200, n is greater than or equal to 225, n is greater than or equal to 250, n is greater than or equal to 275, n is greater than or equal to 300, n is greater than or equal to 325, or n is greater than or equal to 350; for one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal; and generating from the values a quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal by comparing the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown sensory perception in a mammal to the quantitative representation of sensory perception in a mammal for the one or more molecules or combinations of molecules yielding known sensory perception in a mammal. The sensory receptors used in this method may include a receptor disclosed herein, or fragment or variant thereof. The maximum number of taste receptors that are needed to mimic the native repertoire (*e.g.*, about 50) may be less than the maximum number of olfactory receptors that are needed (*e.g.*, about 350). But the number of sensory receptors that need to be represented in an assay to provide useful results may be much less.

Assaying for ligand-receptor binding in a large set of sensory receptors is envisioned to mimic the function of the nose or tongue in sensory perception of chemical sensants. For a set of sensory receptors with a redundancy of ligand-binding domains, the resultant signal is a summation of the interactions of all sensory receptors in the set: none, one, or a few of which have ligand-binding domains that are a perfect fit for the sensant; some of which have ligand-binding domains that are only an imperfect fit for the sensant; and most of which do not significantly bind to the sensant. The individual sensory receptor's binding affinity for sensant varies accordingly. Thus, a suitably large set of ligand-binding domains from sensory receptors will be analogous to any ability of the native repertoire of olfactory or taste receptors to tolerate varying degrees of mismatch between ligand and ligand-binding domain.

The complication of desensitization of sensory receptor signaling will also be avoided by using the invention instead of preparations of nasal or tongue epithelium containing native sensory receptors. For example, the event of binding between ligand and receptor can be separated from more complicated downstream signaling events in the epithelial cells. But the latter events can be reconstituted in the invention by transferring the sensory receptor of interest into appropriate host cells containing an intact and functional signaling pathway.

H. Administration of Novel Sensant Compositions

Sensory modulators can be administered directly to a mammal (e.g., human) for modulation of sensory perception *in vivo*. Administration is by any of the routes normally used for introducing a modulator compound into ultimate contact with the tissue to be treated (e.g., nose or tongue). The olfactory modulators are administered in any suitable manner, optionally with acceptable carriers. Suitable methods of administering such modulators are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route. Acceptable carriers are determined at least in part by the particular components of the composition to be administered (e.g., stabilizing the sensants), as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions of the present invention (see, e.g., *Remington's Pharmaceutical Sciences*, 17th ed. 1985).

The sensory modulators, alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichloro-difluoromethane, propane, nitrogen, and the like that may or may not contribute to sensory perception. Other possible formulation include dry or liquid forms, powders or tablets, solutions of polar (e.g., water) or nonpolar (e.g., alcohol) solvents, emulsions or suspensions, creams, gels, lotions, and syrups.

Formulations suitable for administration include aqueous and non-aqueous solutions, isotonic sterile solutions, which can contain antioxidants; buffers,

I. Kits

Sensory receptor genes, or fragments or variants thereof are useful tools for identifying cells expressing sensory receptors, for forensics and paternity determinations, and for examining signal transduction in isolated cells. Sensory
5 receptor family member-specific reagents that specifically hybridize to sensory receptor nucleic acids, such as AOFLF1 probes and primers, and sensory receptor specific reagents that specifically bind to a sensory receptor protein, *e.g.*, anti-sensory receptor antibodies are used to examine expression in cells and regulation of signal trans-duction. For example, one or more family member-specific reagents may be
10 used to detect poly-morphisms that are linked to genetic anosmia or to detect allelic exclusion.

Nucleic acid assays for the presence of DNA and RNA for a sensory receptor family member in a sample include numerous techniques are known to those skilled in the art, such as Southern analysis, Northern analysis, dot blots, RNase protection, S1
15 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybrid-ization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*,
20 *Biotechniques*, 4:230-250 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, a sensory receptor protein can be detected with the various immunoassay techniques described above. The test sample is typically compared to both a positive control (*e.g.*, a sample expressing a recombinant sensory
25 receptor protein) and a negative control.

The present invention also provides for kits for screening for novel modulators of sensory receptor family members. Such kits can be prepared from readily available materials and reagents, as well as any of the aforementioned products. For example, such kits can comprise any one or more of the following materials: sensory receptor
30 nucleic acids or proteins, reaction tubes, and instructions for testing sensory receptor activity. Optionally, the kit contains a biologically active sensory receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

Examples

AOLFR1 sequences:

- MKTFSSFLQIGRNMHQGNQTTTTEFILLGFFKQDEHQNLFLVFLGMYLVTVVIGNGLIIVAISLD
TYLHTPMYLFPLANLSPADISSINSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLGLTM
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIIALTHTLLQLLFCNHNHTLPHFFCDLAPLL
KLSCSDTLINELVLFVIGLSVIIIFPFLSFFSYVCIIRAVLRVSTQGWKAFTSCGSHLTVVLLFY
GTIVGVYFFPSSTHPEDTDKIGAVLTVVTPMINPIYSLRNKDMKGALRLKLNKISSL (SEQ ID
NO: 1)
- 10 ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAACCA
CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCTCTTT
GTGCTTTTCTTGGGATGTGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTTGTGGCTA
TCAGCTTGGATACGTACCTTCATACCCCATGTATCTCTTCCTTGCCAACTCATCTTTGCT
GATATTTCTCCATTTCACACTCAGTCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC
15 AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTCTATTGTGTTTGTGTCATT
GACAATTTGCTCTTGGGGACCATGGCCATTGACCACTTTGTGGCGATCTGCCACCCCTGA
ATTATACAATTCATCGCGCCAGGTTTCGGCATTTTGTCTACAGCATCTCATGGTTCCTC
AGTAATATTATTGCTCTGACACACACCCCTCTGCTCATCAATTGCTCTTCTGTAACCAACA
CACTCTCCACACTTCTCTGTGACTTGGCCCTCTGCTCAAAGTCTGCTGTCAGATACAT
20 TGATCAATGAGCTGTGTGTGTTATTGTGGGTTTATCAGTTATCATCTTCCCTTTACACTC
AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCTGAGAGTATCTTCCACACAGGGAA
AGTGGAAGGCTTCTCCACTTGTGGCTCTACCTGACAGTTGTATTACTGTCTACGGAAC
CACTGTAGGCGTGACTTTTCCCTCTCTCCACTCACCTGAGGACACTGATAAGATTGGT
GCTGTCTATTCACTGTGGTGACACCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA
25 AGGATAGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCTTTGA (SEQ
ID NO: 2)

AOLFR2 sequences:

- MMMVLRLNSMEPTFALLGFTDYPKLIQPLFLVFLLMYVITVVGNLGMIHIIKINPKFHTPMYFFL
SHLSFVDFCYSSIVTPKLLNLVMAKDSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC
NPLLVTYVAMSQRLCALLVAGSYLWGMFGPLVLLCYALRLNFSGPNVINHFCEYALTISVSGS
DLIPHLLLFSFATFNEMCTLLIILTSYVFIVTVLKIRSVSGRHKAFSTWASHLTATITFIHGHTILF
YCVPSNKSNSRQITVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
3)
- 35 ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCCACTTTGCCCTTTTAGGTTTACAG
ATTACCAAAAGCTTCAGATTCTCTCTCTTGTGTTTCTGCTCATGTATGTATCAAGTG
TGAGGAAACCTTGGGATGATCATAATAATCAAGATTAAACCCAAATTCACACTCTTATGT
ACTTTTTCTTAGTCACCTCTCTTTTGTGTGATTTTGTGTTACTCTTCCATTGTCACCTCCAAGC
40 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGACGTA
CTTCTGCTCTGCACTGCTGTGGTGACAGAGTCTTCTTGTGGCAGTGTGACCTTGTGAC
CGCTTTGTGGCCATCTGAATCCTCTGCTTATACAGTGGCCATGTCACAGAGGCTCTGTG
CCCTGCTGGTGCTGGGTCAATCTCTGGGGCATGTTTGGCCCTTGGTACTCTTTGTTAT
GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTGTGAGTATACTGC
45 TCTCATCTCTGTGCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTCAAGTTCGCCA
CCTTCAATGAGATGTGTACACTACTGATCATCTCTCACTTCTATGTTTTATTGTTGACT
GTACTAAAAATCCGTCTGTGTTAGTGGGGCCACAAAGCCTTCTCCAGTGGCACTGCCACC
TGACTGCTATCAACACTTCTCAATGGGACCATCTTTCTCTTATCTGTTGACCCCACTCAAA
AACTCTCGGCAAAACAGTCAAAGTGGCCTCTGATTTTACACAGTTGTCAACCCCATGCTGA
50 ACCCTCCGATCTACAGCCTAAGGAATAAGAGAGCTGAAGGATGCTTCTGGAAGTAAATACA
TACACAAGTTCCATTCTACTGA (SEQ ID NO: 4)

AOLFR3 sequences:

- MLLTDRTNSGTTTLLGFSDYPELVPLFLVFLAIYNTVLGNIGLIVIIKINPKLHTPMYFFLSQ
LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFTFVVTESFLLAVMAYDRFVAICNP
LTYVDMSQKLCVLLVVGSYAWGVSCSLELTCALKLCFHGPNNTINHFCEFSLLSLSCSDNPTI

NQWLLFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITFHFGLTILFYCV
PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDVTTEILDTKVFSY (SEQ ID NO: 5)

5 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTCAACCTCTTGGGCTTCTCAGATT
ACCCAGAAGTGCAGTCCCACTCTTCTGGTTTCTTGGCCATCTACAAATGCTACTGTGCTA
GGGAAATATGGGTTGATTGTGATCATCAAATCAACCCAACTGCATACGCCCATGTACT
TTTCTCTCAGCCAACTCTCTTTGTGGATTCTGCTATCTCCATCATTTGCTCCCAAGATG
TGGGTGAACCTTGTGTCAAAGACAGAACCATTTTATTTAGGATGCGTAGTACAAATGCT
TTTTCTCTGTACTCTTGGGTCACCTGAATCCTTTTATTAGCTGTGATGGCCTATGACCGC
10 TCTGTGGCCATTTGCAACCCCTCTGCTCTACACAGTTGACATGTGCGCAAGAACTCTCGGTGC
TGCTGGTTGTGGGATCCTATGCTGGGGAGTCTCAIGTTCCTTGGCAAGTACGCTGCTCTGC
TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCTCAC
TACTCTCCTTTCTTGTCTGTACTTACATCAACCAAGTGGCTGCTATCTTTCTTGGCAAC
TTTAAAGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT
15 CCTCAAGATGCGTTTCAGTCAGTGGGCGCCGCAAGCCTTCTCCACCTGTGCGCTCCCACTG
ACTGCCATCACCATCTTCCATGGCACCATCTCTCTTACTGTGTGCCCACTCCAAAAA
CTCCAGGCACACAGTCAAAGTGCGCTCTGTGTTTTACACCGTGGTGATCCCCATGTTGAAT
CCTCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATATGGC
ACCAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

20 **AOLFR4 sequences:**

16MENQNNVTEFILLGLTENLELWKIFS AVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS
LDLVMESSVVAPKIVVDTLKSTTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY
TIMSPRVCLMVGGAWVGGEMHAMIQLLFMYQIPFCGPNIDHFDICDLQFLTACTDTHILGL
25 VTLNLSGMMCVAFELILIASYTVILCSLKSYSKGRHKALSTCSSHLTVVVLFVPCIFLYMRPV
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKLMWKMWEALAGK (SEQ ID NO: 7)

30 ATGGAAAAACAAACAATGTGACTGAATTCATCTTCTGGGTCTCAGAGAGAACCTGGAGC
TGTGGAAAAATATTTCTGCTGTGTTCTTGTGTCATGTATGTAGCCACAGTGTGGAAAAATCT
ACTTATTTGTGGTAACTATTATCAAGTCAAGTGTGAGGTCACTTATGATATTTTCTCTA
CTCTCTGTCCCTTTTGGGATGTCATGTTCTCATCTGTGCTGTGCCCAAGGTGATGTAGAC
ACCTCTCCAAGACACTACCATCTCTCTCAAAGGCTGCTCACCACAGCTGTTGTGGAGC
ATTTCTTGTGGTGTGGGGATCATCTCTCTCACTGTGATGGCCTATGACCGCTACGTGGC
35 CATCTGTAAAGCCCTGCACTACAGATCATCATGAGTCCACGGGTGTGCTGCCATATGGTA
GGAGGGGCTGGGTGGGGGATTTATGCAACGCAATGATACAACCTCTCTTCAATGTATGATAA
TACCTTCTGTGGTCTTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA
CTTGCTGCACGGACACCCATCTCTGGGCTCTTAGTTACCTCTCAACAGTGGGATGATGT
GTGTGGCCATCTTCTTATCTTAAATTGCTTCAACCGTCACTATGCTCTCCAGAGTCT
TACAGCTCTAAAGGCGCGCAAAAGCCCTCTCTACCTGCAAGTCCCACTCAGCGTGGTTG
40 TATTGTTCTTTGTCCCTGTATTTTCTGTGATACAGGCTGTGGTCACTACCCAGATAAG
AAGGCAATGGCTGTGTGAGACTCAATCATCACCCATGTTAAATCCTTGATCTATACAC
TGAGGAATGCAAGGTGAAAAAGTGCCATGAAGAAACTCTGGATGAAATGGGAGGCTTGG
CTGGGAAATAA (SEQ ID NO: 8)

45 **AOLFR5 sequences:**

17MGKENCTTVAEFLILLGLSDVPPELVCLFLFLLIYGVTLLANLGMIALIQVSSRLHTPMYFFLSH
LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVTEVFLVAMAYDRFVAICNPL
LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLAIRPFYRNSVINHFCDLPPVLSLACSDITVN
ETLFLVATL NESVTIMILTSYLLILTLTKMGS AEGRHKAFTSCASHLTAITVFHGTVLSIYCRP
50 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKALRKMVMSKIH (SEQ ID NO: 9)

55 ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCACTTCTCTTGGACTATCAGATGTCC
CTGAGTTGAGAGTCTGCCTCTTCTGCTGTCTCTCTCATCTATGGAGTCACGTTGTAGGC
AACCTGGGCATGATTGCACTGATTACAGTCACTCTGGCTCCACACCCCAATGACTTTT
TCTCCAGCACTGTCTCTGTAGATTCTGCTACTCTCAATAATTTGGTCCCAAGATGTTG
GCTAATATCTTTAACAAGGACAAAGCCATCTCTTCTAGGGTGCATGGTGCAATTTACT

TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCTGCTGGCCGTGATGGCCTATGACCGCTT
 GTGGCCATCTGTAACCCCTTGTCTATACACAGTCACCATGTCTTGAAGGTGCGTGTGGAGC
 TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTGTGCTTAGCTCTT
 AGGATCCCCCTTCTATAGATCTAATGTGATTAACCACTTTTCTGTGATCTACCTCTGCTCT
 5 AAGTCTTGTCTGCTGTGATACATCTGTGAATGAGACACTGTGTTCTGGTGGCCACTTTG
 AATGAGAGTGTTACCATCATGATCATCTCTACCTCTACCTGCTAATTCTCACCACCATCTC
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCACCTCACA
 GCTATCACTGTCTTCCATGGAACAGTCCCTTCCATTTATTGCAGGCCAGCTTCAGGCAATA
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTTGTCTGAATCTC
 10 TGTGATCTACAGCTTGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
 CAAAATCACTCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

MMASERNQSSPTFILLGFSEYPEIQVPLFLVFLVYTVTVVGNLGMIIIRLSNKLHNTIMYFFLS
 15 HLSLTDFCSTVVPKLENNLVVEYRTISFSGCIMQFCACIFGVTEFMLAAMAYDRFVAVCK
 PLLYTTMSQKLCALLVAGSYTWGIVCSLILTYFLDLLSFCESTFINNFICDSHVIVSASYSYDPS
 QRLCFIAIFNEVSSLIIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTATIFHGTILFLYCVPNP
 KTSSLIVTVASVYTVVAIPMLNPLIYSLRNKDINNMEKLVVTKLIYH (SEQ ID NO: 11)
 20 ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATCTCTCTGGGTTTTTCAG
 AATACCCAGAAATCCAGGTTCCACTCTTCTGGTTTTCTGTTCGTCTACACAGTCACTGTGA
 GTGGGGAACCTTGGGCATGATAAATATCATCAGACTCAATTCAAACCTCCATACATCAATGAT
 ACTGTTTTCCCTAGTCACTGTCTTGACAGACTTCTGTTTTCCAGCTGAGTTACCACTAAAG
 CTGTTGGAGAACCTTGGTTGTGGAATACAGAACCATTCTTCTCTGGTGCATCATGCAAT
 25 TTTGTTTTGCTTGCATTTTGGAGTGCAGAAACTTTCATGTTAGCAGCGATGGCTTATGAC
 CGTTTTGTGGCAGTTTGTAAACCTTGTCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC
 TCTTCTGGTGGGTGGGTCTATACATGGGGGATAGTGTGCTCCCTGATACTACATATTTT
 CTCTTGACTTATCGTTTTTGTGAATCTACCTTCATAAAATAATTTATCTGTGACCACCTGT
 AATTGTTTCTGCCTCTACTCAGACCCTATATCAGCCAGAGGCTATGCTTTATTTATTTGCCA
 30 TATTCAATGAGGTGAGCAGCCTAATTATCATCTTGACATCATATGCTTATTTTCACTACC
 ATTAAGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCTCTCCACC
 TGACAGCCATCACTATTCTCAATGGAACATCTCTTTTCTTACTGTGTTCTCAATGCTAA
 ACTTCTAGCCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
 ACCCATGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
 35 CACCAAAATTGATTTACCACTGA (SEQ ID NO: 12)

AOLFR7 sequences:

MSYFYRLKLMKEAVLVKLPFTSLPLLQLTSLSRKSRDEIKNYSSTSGFILLGLSSNPQLQKPLF
 AIFLIMYLLAAVGNVLIIPIAYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLETKVVISY
 40 VGCLAQMYYFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGCSCISHLHL
 FRVLLMSRLVSFCAASHIHKHFFCDTPQVPLKLSCDSTSSSQMVMTETLAVIVTFFLCIIFSYLRIMV
 TVLRIPSAAGKWKAFSTCGSHLTAVALFYGSIIYVFRPLMSYSVVRDRVATVMTYVTVPMPLN
 PFYSLRNKDKRGLKLQDRIYR (SEQ ID NO: 13)
 45 ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA
 CATCTCTCCCACTCTTCTCCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
 CTACAGCAGCAGCAGCTCAGGCTTCTATCTCTGGGCTCTCTTCCAAACCTCAGCTGCAG
 AAACCTCTCTTTGGCACTTCTCTCATCATGTACTGTCTGCTGCGGTGGGGAATGTGGCTCAT
 CATCCCGGCATCTACTCTGACCCAGGCTCCACACCCCTATGTACTTTTTCTCAGCACT
 50 TGTCTTTATGGATATCTGCTTCAACACAGTCATAGTGCCTAAGATGCTGGTGAATTTCTA
 TCAGAGACAAAGGTTATCTCTATGTGGGCTGCCTGGCCAGATGTACTTCTTATGGCAT
 TTGGGAACCTGACAGCTACCTGCTGGCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
 CAACCCCTTACATCATGATGTGGTTATGAAACCACGGCAATTCGCTGCTATGCTATTGGGT
 TCTTGCAGCATCTCCCACTACATTCCCTGTTCCGCGTGTACTTATGTCTGCTTGTCTT
 55 CTGTGCTCTCATCATTAAGCACTTTTCTGTGACACCCAGCTGTGCTGAATAAGCTCTCTCT
 GCTCTGACACATCTCCAGCCAGATGGTGGTGTACTGAGACCTTAGCTGTCAATTGTGAC

5 CCCCTTCCTGTGTATCATCTTCTCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCCT
CTGCAGCCGGGAAGTGGAAAGCCCTTCTCTACCTGTGGCTCCCACCTCACTGCAGTAGCCCT
TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTACTCAGTGGGTAGGG
ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTTCATCTACAG
CCTGAGGAACAAGAATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
A (SEQ ID NO: 14)

AOLFR8 sequences:

10 MATSNHSSGAEFILAGLTQRPELQLPLFLFLGIYVVTVVGNLGMIFLIALSSQLYPPVYFLSH
LSFIDL CYSSVITPKMLNVFVPEENISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPILY
NIVMSHRVCSIMMAVVYSLGFLWATVHTTMRMSVLSFCRSHTVSHYFCDILPLLTLS CSSHTHINEI
LLFIIGVNTLATTLAVLISYAFIFSSILGHSSTEGQSKAFGTCSSHLLAVGIFFGSITEMYFKPPSS
TTMEKEKVS VFYITIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

15 ATGGCTACTTCAAACCACTTCTCAGGGGCTGAGTTTATCTCGCAGGCTTGACACACGCC
CAGAACTTCAACTGCCCACTTCTCTCTGTTCCTTGGAAATATATGTGGTCACAGTGGTGGG
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTACCCTCCAGTGATATTAT
TTCTCAGTCATTGTGCTTTCATTGATCTCTGCTACTCCTCTGTCAATTACCCTTAAGATGCTG
GTGAACCTTGTTCAGAGGAGAACATTATCTCCTTCTGGAATGCATTACTCAACTTATTT
20 CTTCCTTATTTTGTAAATGCGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
GTGCTATCTGTCGCCCACTGCTTACAATATTGTCATGTCCCACAGGGTCTGTTCCATAAT
GATGGCTGTGGTATACTCACTGGGTTTCTGTGGGCCACAGTCCATACTACCCGCATGTGA
GTGTGTGCTATCTGTAGGTCTCATACGGTCAGTCATTATTTTGTGATATTCTCCCTTATT
GACTCTGCTTGTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTCATTATTTGGAGGAGTT
25 AATACCTTTAGCAACTACACTGGCGGTCCTTATCTTATGCTTCACTTCTCTAGTATCTT
TGGTATTCACTCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGTAGCTCCCATCTCTGTG
GCTGTGGGCATCTTTTGGGTCTATAACATTCATGATATTTCAAGCCCTTCCAGCATAC
TATGGAAAAAGAGAAGGTGCTTCTGTGTTCTACATCAACAATAATCCCATGCTGAATCCT
30 CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
AGGCAGTCATCTGA (SEQ ID NO: 16)

AOLFR9 sequences:

35 MLARNNSLVTEFILAGLTDRPEFWQPFFFLFLVIYIVTMVGNLGLITLFLGNSHLHTPMYYFLFN
LSFIDL CYSSVITPKMLNVFVSKKNISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
LYKV TMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANHNYLCDILPLLQLSCTSTYV
NEVVVLVVGNTIVPSTILISYVFI VTSILHIKSTQGRSKAFSTCSSHVLIALSFFGSAAFMYIKY
SSGSMEQKGVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRNIF (SEQ ID NO: 17)

40 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATCTTGTCTGGATTACAGATCGTC
CAGAGTTCTGGCAACCCCTCTTTTCTCTGTCTAGTGATCTACATTGTCACCATGGTAGGC
AACCTTGGCTGTGACTACTTTCGTTCTAAATTTCAACCTCCACACACCAATGACTATT
CCTCTCAACTCTCTCTTCAATTGATCTCTGTTACTCCTCTGTTTCACTCCCAAAATGCTAAT
GAACTTTGTGTGCAAAAAGAATATTATCTCCAATGTGGGTGCATGACTCGGCTGTTTTCT
TTTCTCTTTTCGTCACTCTGTAATGTTACATGTTGACCTCAATGGCATATGATGCTATGT
45 GGCCATCTGTAATCCATTGCTGTATAAGGTACCATGTCCCATAGGCTCTGTTCTATGCTCA
CTTTTGTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAC
ACTCACTTCTGCAAGTGCTAATATCATTAAACCATTACTTGTGTGACATATCCCCCTCTCTC
AGCTTTCTGCAACGACCACTATGTCAACGAGGTGGTGTCTCATGTTGTGGGTACTAA
TATCACGGTAGCCAGTTGTACCATCTCATTCTTATGTTTCACTGTGCACTAGCATCTTCT
50 ATATCAAAATCCCACTCAAGGAAGATCAAAAGCCTTCACTGACTGTAGCTCTCATGCTATGC
TCTGTCTCTGTTTTTGGGTGAGCGGCAATCATGATATTAATAATTTCTTGGATCTATGG
AGCAGGGGAAAAGTTTTTCTGTTTCTACATAATGTGGTGCCCATGCTCAATCCCTCATC
TACAGTTTGGAGAACCAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAATAATTCAG
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

55

AOLFR10 sequences:

MLARNNSLVTEFLLAGLTDREPRQLFFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFNL
SFIDL CYSSVFTPKMLMNFVSKKNIIISVVGCMTQLFFFLFFVISECYILTSMAYDRYVAICNPLLY
KVTMSHQVCSMLTFAAYIMLAGATAHTGCMRLRTFCSANIINHLYLCDILPLQLSCTSTYVN
5 EVVVLIVVGINMVPSCITLISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS
SGSMEQKGKVSSVFYTNVPMNLNPLIYSLRNKDVKVALRKALIKIQRNRIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATCTTGTGCTGGATTAACAGATCGTC
CAGAGTTCCGGCAACCCCTCTTTTCTGTTTCTAGTGATCTACATTGTCAACCATGGTAGGC
10 AACCTTGGCTTGATCATCTCTTTCCGCTCAAATCTCACTCCACACACCAATGTACTATT
CCTCTTCAATCTCTCTCTCATTTGATCTCTGTACTCCTGTGTTTCACTCCCAAAATGCTAAT
GAACCTTGTATCAAAAAAGAATATATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTTCT
TTCTCTTTTTTGTCTCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
GCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTTCTATGCTCAC
15 TTTTGTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACGGGTGCATGCTTAGA
CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATCTCCCCCTCTCCCA
GCTTCTCTGCACCAAGCACTATGTCAACGAGGTGGTGTGTTCTCATGTTGTGGGATTAAT
ATCATGGTACCCAGTTGTACCATCTCTCAATTTCTATGTTTTCATTGTCACTAGCATCTTCA
TATCAAAATCCACTCAAGGAAGATCAAAAGCCTCAGTACTGTGAGCTCTCATGCTATTGCT
20 CTGCTCTGTGTTTTTGGGTGAGCGGCATTCTGTATATTAATAATTTCTTGTGATCTATGGA
GCAGGGAAGAAGTTTCTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCT
ACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAATAATTCAGA
GAAGAAATATATTCTAA (SEQ ID NO: 20)

AOLFR11 sequences:

MTLRNSSSVTEFILVGLSEQPELQLPLFLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLNL
FIDL CYSCVFTPKMLNDFVSEIISVVGCMTQLFFFCFFVNSECYVLVSMAYDRYVAICNPLLY
MYTMSPRVCFLLMFGSVVVGAGAMAHTGSMRLTFCDSNVIDHYLCTDVLPLQLSCTSTHV
30 SELVFFIVVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSIIAVALFFGSGTFTYLTTS
FPGSMNHGRFASVFTYTNVPMNLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTGGGATTATCAGAACAGC
CAGAGCTCCAGCTCCCTCTTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
AACTTGGGCTTGATCACCTTAATTTGGGATAAATCCTAGCCTTCAACCCCCATGTACTTTTT
35 CCTCTTCAACTTGCTCTTATAGATCTCTGTTATCTCTGTGTGTTTACCCCAAAATGCTGA
ATGACTTTTGTTTTCAGAAAGATCATCTCTTATGTGGGATGATGACTCAGCTATTTTTCTTC
TGTTTCTTTGCTCAATCTGAGTGCTATGTGTTGGTATCAATGGCCATGATCGCTATGTGGC
CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCCAAGGGTCTGCTTTCTGCTGATGT
TTGGTTCTATGTGGTAGGGTTTGTCTGGGGCCATGGCCACACTGGAAGCATGCTGCGACT
40 GACCTCTGTGATTTCCAAAGCTCATTGACCATATCTGTGTGACGTTCTCCCCCTCTGCAGC
TCTCTGCACCAAGCAACCATGTCAGTGAGCTGGTATTTTCTATGTTGTGGAAGTAAACAC
ATGCTATCCAGCATAAAGCATCGTCATCTCTTACGCTTGTATCTCTTCAACATCTCTGTAT
TGCTTCTGCAGAGGGCAGATCAAAAGCCTTTAGCACATGGGGCTCCCACATAATTTGCTGTT
GCTCTGTTTTTGGGTGAGGACATTACCTACTTAACAACATCTTTCTTGGCTCTATGAA
45 CATGGCAGATTTGCTCAGTCTTTTACACCAATGTGGTGTCCCATGCTTAACCCCTCGATCT
ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCGAAAGAGAGTGCTCT
TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

MERNHNPDNCNVLNFFADKKNKRRNFGQIVSDVGRCYSVLSLGEPTMTGRNNLRTPSEFIL
LGLSSRPEDQKPLFAVFLPIYLTIVIGNLLIILAIRSDTRLQTPMYFFLSLFSVDICYVTVIIPKMLV
NFLSETKTSYGECLTQMYFFLAFGNTDYSYLLAAMAIIDRYVAICNPFHYTIMSHRCCVLLPVS
FCIPHHSLLHITLNLQIFCASNVIIHFFCDDQPVVLKSCSSHVFKEITVMTTEGLAVIMTPPSCII
50 SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVVFQPLSNYTVKDKIATIIYTVLTP
MLNPFYIYSLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

ATGGAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTCTTTGCTGATAAGA
AGAATAAAAGGAGAAATTTTGGACAGATTGTATCAGATGTTGGAAGAAATCTGTTACAGTG
TTAGTTTATCTTTAGGTGAACCCACAACATATGGGAAGAAATAACCTAACAGACCCCTGTGA
ATTTCATCTCTCTTGACTCTCTCTCAGCTGAGGATCAGAAGCCGCTTTTGCTGTGTCC
5 TCCCCATCTACCTTATCAGACAGTGATAGGAAACCTGCCTTATCATCTGGCCATCCGCTCAGA
CACTCGTCTCCAGACGCCATGTACTTCTTCTAAGCATCTCTGCTTTTGTGTGACATTGTCT
ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACITCTTATCAGAGACAAAGACCATCTC
TTACCGTGTAGTGCTGACCCAGATGTACTTTTCTTAGCCTTTGGAAACACAGACAGTTAC
10 CTGCTAGCAGCTAGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCATACATCA
CCATTATGAGTACAGATGCTGTGCTGCTCTGCTTCTGCTTCTGCTCCCAATGTCATCCA
CACTCCCTCTGCACATCTTCTGACTAATCAGCTCATCTTCTGTGCTCCCAATGTCATCCA
TCACTTTTCTGCGATGATCAACCAAGTGCTAAATTTGCTGTTCTCCCTTTTGTCAAAG
AAATCAGATAATGACAGAAAGGCTTGGCTGTCAATAAGACCCGCTTTTCATGCATCATCAT
CTCTTATTTAAGAATCTCATCACTGTCTGAAGATTCTTCAGCTGCTGGAAAGCGTAA
15 GCATTTTCTACCTGTGGCTCTCATCTCAGAGTGGTGACCCGTGTTTATGGAAGCATTAGCTA
TGCTATTTTACGCCCTGTCCAACATACTGTCAAGGATCAAAATGCAACAATTATCTAC
ACCGTACTGACTCTATGCTAAATCCATTATCTATAGTCTGAGGACAAAGACATGAAGC
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

20 **AOLFR13 sequences:**

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFLLGNKTHIVLSHLDPHLHNPMMYFFSNL
SFIDLCTYTTGIHPQLLNLNRGADKSISYGGCVVOLYISLGLGSTCEVLLGVMAFDRTAAVCRPL
HYTVVMHPCLVYVMASTSWVIGFANSLLOTVLILLTLGRNKLEHFLCEVPPLLKLCACVDTT
MNESELFVSVIILLVPVALIIFSYSQIVRAVRIKSA TGQRKVFGTCSHLLTVSVLFGYTAAAY
25 LQPGNNYSQDGKXISLFYTHITPMINPLIYTLRNKDVKALKKVLWKNYDSR (SEQ ID NO:
25)

ATGGATCAGAAAAATGGAAGTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC
CTCAGCTGGAGCTAGTCTCTTTGTGGTGTATTGATCTTCTATATCTTCACTTTGCTGGGG
30 AACAAAAACCATCTGTTATTATCTCACTTGGACCCACATCTTCAACAATCCTATGTTATTTT
CTTCTCCAACCTAAGCTTTTGGATCTGTGTACACAACCGGCATTGTTCCACAGCTCCTGG
TAAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAAGCTGTACAT
CTCTCTAGGCTTGGGATCTACAGAAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
GCAGCTGTTTGCAGGCCCTCCACTACACAGTAGTCAATGACCCCTTCTGTATGTGCTGA
35 TGGCTTCTACTTCAATGGCTCATTGGTTTGGCAACTCCCTATTGACAGCGGTGCTCATCTTG
CTTTAAACATTTTGGGAAGAAATAAATAGAACACTTCTTGTGAGGTTCTCCATTTGCT
CAAGCTTGCTGTGTTGACACTACTATGAATGAATCTGAACCTTCTTTGTGAGTGTCAATTA
TTCTCTTGTACCTGTGCTAATCATATTCTCTATAGTCAGATTGTGAGGGCAGTCCGTG
AGGATAAAGTCAGCAACAGGGCAGAGAAAGTGTTTGGGACATGTGGCTCCCACTTCAGA
40 GTGGTTTCCCTGTCTACCGGCACAGCTATCTATGCTACCTCCAGCCCGGCAACAACATCTC
TCAGGATCAGGGCAAGKTCATCTCTCTCTACACCATCATACCCATGATCAACCTC
CTCATATACACTGAGGACAAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
AACTACGACTCCAGATGA (SEQ ID NO: 26)

45 **AOLFR14 sequences:**

MALPILLSPSCFASQSLSSRMNSENLTRAAPAEEFVLLGITNRWDLRVALFLTCLPVVYLVS
LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSSAIGPKMLVDLLPRATIPYATACALQMF
VFAGLADTECCLLAAMAYDRYVAIRNPLLYTAMSQRLCLALLGASGLGGAVSAFVHTLTFT
RLSFCRSRKINSFFCDIPLLAISCDSTLSNELLFALCIGFIQTATVLAITVSYGFIAGAVIHMSVE
50 GSRRAASTGSHLLTAVAMMYGTLIFMYLRPSSSYALDDTKMASVFYTLVPSLNPLIYSLRNKE
VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

ATGGCCTTGCCATTGCTCTTATCTCCCTCTGCTTTGGCTCTTCTCAGTCTCTGTCCAGTAG
GATGAACCTCAGAGAACTACCCGGGCGCGGTGCGCCCTGCTGAATCTGCTCTCTCTGGGC
55 ATCACAAACTGCTGGGACCTGCGTGTGGCCCTCTTCTGACAGCTGCTGCTGCTGCTACCTGG
TGAGCTCTGCGGAAACATGGGCATGGCCTGCTGATCCGATGGATGCCCGGCTCCACA

- CACCTATGTACTTCTCTGGCCAACTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATL
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCGAGCCACCTTACACAGCCTGTG
CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTGCTTGCTGGCAGCAT
GGCCTATGACCCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAAACAGTATGTCCGAG
5 CGTCTATGCTTCCGCTTCTGCTGGGAGCATCAGGCTGGGGTGGGCGAGTGAGTGCTTTGTTC
ACAAACCCCTCACTTCCGCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG
CGATATCCCTCCACTGTCTGGCCATCTCGTGCACTGACACCACTCTCAATGAACTCTTCTCT
TCGCCATCTGTGGCTTATCCAGACAGCCACGGTGTAGCTATCAGCGTGTCTTATGGCTT
CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGCGAGGCGAGTCGGCGAGCGCTCCAC
10 CGGTGGTTCCCACTCAGCCGTGGCCATGATGTACGGGACACTATTTTATGTACCTG
CGCCCCAGCTCCAGTATGCCCTGGACACTGACAAGATGGCCTGTGTCTTATACCTG
TCATCCGCTCTCAACCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGCCGATTCACCTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)
- AOLFRI5 sequences:**
MRENNQSSLEFILLGVGTQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNPMYFLLANLS
LVDIFFSSVTPKMLANHLGSKSISFGGCLTQMYFMIALGNLTDVILAAMAAYDRAVAISHPLH
YTTIMSPRCIWLIIAGSWVIGNANALPHLLTASLSFCGNQEVANFYCDITPLLLKSCSDIHFIHV
KMMYLGVGIFSVPLLCIIIVSYIRVSTVFQVPSTKGVLKAFSTCGSHLTVVSLYYGTVMGTIFYR
20 PLTNYSLKDAVITVMYTA VTPMLNPFYISLRNRDMKAALRKLFNKRIS (SEQ ID NO: 29)
- ATGAGGAAAAATAACCACTCTCTACCTGGAATTCATCTCTCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTCTCTACATCCTCTCTGTTCTATTACCCCACTGATTGTGGA
AACCCTGCTACTTGTCTAGCCATTTGCTCTGATGTTTCGCCCTTCAACAACCCATGTATTTCT
25 CCTTGCCAACTCTCTTGGTGGACATCTTCTCTCATCGGTAAACCATCCCTAAGATGCTCGG
CCAACTATCTCTGGGCGAGCAATCCATCTCTTTGGGGGATGCCTAACGCAATGTATTT
CATGATAGCCTTGGGTAAACAGACAGCTATATTTGGTGCATAGCATATGATCGAGCT
GTGGCCATCAGCCACCACTTCACTACACAACAATATGAGTCCACGGTCTTGATCTGGC
TTATGCTGGGTCTTGGGTGATTGGAATGCAATGCCCTCCCCCACTCTGCTCAGACG
30 TAGTCTGCTCTTCTGGGCAACAGGAAGTGGCCAACCTTCTACTGTGACATTAAACCCCTG
CTGAAGTTATGCTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTGGCA
TTTGTCTGTGCGATTACTATGCATCACTTGTCTCTATTCGAGTCTTCCCACTGCTTCC
AGGCTCTTCCACCAAGGGCGTGTCAAGGCCTTCTCCACTGTGGTCCCCACTACCGGT
TGTCTCTTGTATTATGGTACAGTCACTGGGCACGTATTTCCGCCCTTTGACCAATATAGCC
35 TAAAGAGCGCAGTGATCACTGTAATGTACAGCGCAGTGACCCCAATGTTAAATCCTTTCAT
CTACAGTCTGAGAAATCGGCACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)
- AOLFRI6 sequences:**
MRRNCTLVTEFILLGLTSRRELQILLFTFLAIYMTVAVAGNLMIVLIQANAWLHMPMYFFLSH
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVCYLFIALVHVIEYILAVMAFDRYMAICNPL
YGRSMKSVCSFLITVPVYVGALTGLMETMWYTNLAFCGPNEINHFCADPLLIKACSDTYN
KLSMFIWAGWNLSFLFIICISYLIYFPAIKIKIRSTEGRKAFSTCGSHLTVATIFYATLFFMYLR
PPSKESVEQGMVAVFYTTVPMNLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)
- 45 ATGAGAAGAACTGCACGTTGGTGACTGAGTTCATTCTCTGGGACTGACCAGTCGCCGG
GAATACAAATCTCTCTTACGCTGTTTCTGGCCATTACATGGTCAGGTTGGCAGGGA
ACCTTGGCATGATTGTCTCATCCAGGCCAACGCTCCACATGCCATGTACTTCTTCT
CTGAGCCACTTATCCCTCTGTGGATCTGTGCTTCTTCCAATGTGACTCCAAAGATGTGCG
50 AGATTTCTTTTTCAGGAAGAAAAGCAATTCTCTATCTCGCTGTCTGTCAGTGTTTACCT
TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCTTTAGCCGGTACAT
GGCCATCTGCAACCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGCTGCTCTTCTC
ATCACGGTGCCTTATGTGTATGGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT
55 TAAGCTGGCTTGTCTGACACCTACAAAGGAGTGTGAATGTTGTTATTTGGTGGCTGGCTGT
AACCTTTCTTTTCTCTCTCATATGATTTCTACCTTTACATTTTCCCTGCTATTTTA

AAGATTTCGCTCTACAGAGGGCAGGCAAAAAGCTTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCCTTTTCTCATGTATCTCAGACCCCTCAAAGGAATCT
GTTGAACAGGGTAAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGTGTAACCTTA
TAATTTATAGCCTTAGAAAAATAAATGTAAAAAGAAGCATTATCAAAGAGCTGTCAATGA
AGATATACTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

MLNFTDVTEFILLGLTSRREWQVLFIIIFLVVYITMVGNGIMMVLKIVSPQLNPNMYFFLSHLS
FVDVWFSSNVPKMLENLFSDKKTITYAGCLVQCFFIALVHVEIFILAAAFDRYMAIGNPLL
YGMKMSRVVNCIRLITFPYIYGLTSLAATLWTYGLYFCGKIEINHFCYADPLIKMACAGTFVKE
YTMILAGINFYSLTVIIISYLFILAILMRSAEGRKAFSTCGSHLTAVIIFYGTLLFMYLRRPTE
ESVEQKGKMAVFYTTVPMPLNPMIYSLRNKDVKKAMMKVIRSRC (SEQ ID NO: 33)

ATGCTCAATTTACCCGATGTGACAGAGTTCACTCTTTTGGGGCTAACGAGCCGTCGAGAAT
GGCAAGTCTCTCTTTCATCATCTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTAAATCAAGGTCAGTCCTCAGCTTAACAAACCCCATGTACTCTTTTCTCTCA
GTCATCTGTCAATTGTGTGATGTGTGGTCTTCTTCCAATGTCAACCCCTAAAAATGTTGAAAAAC
CTGTTTTGAGATAAAAAACAATTACTTATGCTGGTGTGTTAGTACAGTGTCTCTCTTCAT
TGCTCTTTCAGATCATGTGGAAATTTTATTCTTGTCTGCGATGGCCTTGTAGATACATGGCAA
TTGGGAATCCCTTGCTTTATGGCAGTAAATGTCAAGGGTGTGCTGTTTCTGACTGATTCA
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGAAAAAATTGAGATCAACCAATTCTACTGTGACAGTCCACCTCTCATCAAAAT
GGCCTGTGCGGGACCTTTGTAAAGAATATACAAATGATCATACTGCGCGGACCTTAACGCTC
ACATATTTCCCTGACTGTAAATTATCATCTCTTACTTATTCATCCTCATGTGCCAATCTGCGAAT
GCGCTCAGCAGAAGGAAGGCAGAAGGCCCTTTCCACATGTGGGTGCCATCTGACAGCTGT
CATTATAATTCTATGGTACTCTGATCTTATGTATCTCAGACGTCCACAGAGAGGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTTAA (SEQ ID NO: 34)

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVVYLVTLGNLGMIMLMRLDSRLHTPMYFFLT
NLAFVDLCYTSNATPQMSSTNIVSEKTSIFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFLRFTCRSNVINHFYCADPLIKLSCSDTYVK
EHAMFISAGFNLSSSLITVLVSYAFLAAILRIKSAEGRHKAFTCGSHMMAVTLFYGTLCFMYI
RPPTDFTVEESKIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

ATGTCCAACAAAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGGC
CGGAACTCCAGTCTCGTCTTTTGTGCTGTTTCTGTTGTTTACCTCGTCACCCCTGCTAGGC
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTGTGCTATACATCAAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTCTCTTTGCTGGTGTCTTACACAGTGCTACATT
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCCGATATGT
GGCCATATATGACCCCTCTGCGCTACAGTGTGAAAAACGTCCAGGAGAGTTTGCATCTGCTTG
GCCAATATTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCACTTGACCTTCCG
CCTGACCTTCTGTAGATCCAATGTCAATCAACCACTTCTACTGTGCTGACCCGCCGCTCATTA
AGCTTTCTTTGTTCTGATACCTTATGTCAAAGAGCATGCCATGTTCAATATCTGCTGGCTCAAC
CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCTATGCCCTCATCTTCTGCTGCCATCCTCCG
GATCAAAATCAGCAGAGGGGAAGGCAAGGCATTCTCCACCTGTGGTTCCTCATATGATGGC
GTGTCAGTCTGTTTATGGGACTCTCTTTTGCATGTATATAAGACCAACCAAGAGATAAGACT
GTTGAGGAATCTAAAAATAAGCTGTCTTTTACACCTTGTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAGATGTGAAGCAGGCCTTGAAGAATGTCTGAGATGA
(SEQ ID NO: 36)

AOLFR19 sequences:

METKNSYSSSTSGFILLGLSSNPKLQKPLFAIFLIMYLLTAVGNVLILAIYSDPRLHTPMYFFLSNL
SFMDICFTTVIVPKMLVNFLETKIISYVGLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
YDVVMKPPWHCLLMLLGSCSHLSLFRVLLMSRLSFCASHIHKHFFCDTQPVLLKLSCDSTSSSQ
5 MVVMTETLAVIVTFLCTIFSYLQHVTVLRIPSAAGKWKAFTSCGSHLTVVLYFGSVIYVYFR
PLSMYSVMKGRVATVMYTVTPMLNPFYISLRNKMDMKRGLKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCGCTCTCTTCCA
ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCTCATCATGTACCTACTCACTGCGGTG
10 GGGAAATGTGCTCATCATCTCGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT
TTTTCTCAGCAACTGTCTTTTCATGGATATCTGCTTCAACAAGCTCATAGTGGCTAAGATG
CTGGTGAAATTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT
ACTTCTTCATGGCATTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
15 CTCATGCTATTGGGTTCTTGCAGCATCTCCCACTACATTCCTGTTCCGCGTCTACTTAT
GTCTCGCTTGCTTTCTGTGCTCTCACATCATTAAAGCACTTTTCTGTGACCCAGCCTG
TGCTAAAGCTCTCTGCTGTGACACATCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
AGCTGTCATTGTGACCCCTTCTGTGTACCATCTTCTCCTACCTGCAAACTCATCTGCACTG
TGCTCAGAAATCCCCTTGCAGCCGGGAAGTGAAGGCCCTTCTACTCTGTGGCTCCCACT
20 CACTGTAGTGGTCTGTTCTATGGGAGTGTCACTATGTCTATTTTAGGCCCTCTGTCATGT
ACTCAGTGATGAAGGGCCGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
ACCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAGGGGTTGAAGAAATTAAGAC
ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

MVEENHTMKNEFILTGFTDHPKLTLLFVVFAIYLITVVGNSLVALIFTHCR LHTPMYIFLGN
LALVDSMCACAITPKMLENFFSEGRISLYECAVQFYFLCTVETADCFLLAAVGYDRYVAICNP
LOYHIMMSKLLCIQMTTGAFIAGNLHSMIHVGLVFRVFCGLNHNHFVCDTLPRLYRLSCVDFP
INELVLFIFSGSVQVFTIGSVLISYLYLLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP
30 NLEEGGNDIPAAILFTIVVPLNPFYISLRNKEVISVLRKILLKIKSQGSVYNK (SEQ ID NO: 39)

ATGGTGAAGAAAATCATACCATGAAAATGAGTTTATCCTCAGAGGATTTACAGATCAC
CTGAGCTGAAGACTCTGCTGTTGTGGTGTCTTTGCCATCTATCTGATCACCCGTGGTGGG
GAAATATAGTTTGGTGGCACTGATATTTACACACTGCGGCTTCACACCAAACTGACATC
35 TTTCTGGGAAATCTGGCTCTTGTGGATTCTGCTGTGCTGTGCTATTACCCCAAAATGTT
AGAGAACTCTTTCTGAGGGCAAAGGATTTCCTCTATGAATGTGCAGTACAGTTTTAT
TTTCTTTGCACTGTGGAACATGCAGACTGCTTTCTTCTGGCAGCAGTGCCCTATGACCGT
ATGTGGCCATCTGCAACCCCACTGCAGTACCACATCATGATGTCCAAGAAAACCTGCAATCA
GATGACCAAGGCGCTTCATAGCTGGAATCTGCATTCATGATTCATGATAGGGCTTGTA
40 TTAGGCTAGTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATCTCTCCCTT
GTATAGACTCTCTGCTGTGTGACCTTTCATCAATGAAGCTGTTCTATTCATCTCTCAGGTT
CAGTTCAAGTCTTTACCATAGGTAGTGCTTAATCTTATCTATCTCTATCTCTTACTATT
TTCAGAAATGAAATCCAAGGAGGAAGGGCCAAAGCCTTTTCTACTGTGATCCCACTTTT
CATCAGTTTCATTATCTATGGAATCTATTTTCTCTATACATAGACCAAAATTTGCTTGA
45 GAAGGAGGTAAATGATATACCAAGCTGCTATTTTATTAACATAGTAGTTCCTTCAATAATC
CTTTCAATATAGTCTGAGAACAAGGAAGTAATAAGTGCTTAAAGAAAAATTTCTGCTGAA
AATAAATTTCTAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVDFVLLGFTQNPKEQKVLVFMFLFYLLTMVGNLLIVTVTVSETLGSMPSSFFLAGL
TFIDIYSSSISPRLSIDLFFGNNSISFSQSFMAQLFIEHFGGSEVFLLLVMAYDRYVAICKPLHYLV
IMRQWVCVLLVVSVMVGGFLQSVFLSIYGLPFCGPNVIDHFFCDVMYPLLLKACDTHVIGLL
VVRANGSLCTIAFLLLLSYGVILHSLKLLSQKGRQKAHSTCSHITVYVFFVPCIFCMCARPAR
50 TFSIDKSVSVFYTVITPMLNPLYLTRNSEMTSAMKLL (SEQ ID NO: 41)

5 ATGGAGCCAAGGAAAAATGTGACTGACTTTGTCTCTTGGGCTTCACACAGAATCCAAAG
 GAGCAGAAAGTACTTTTTGTATGTTCTTGCTCTTCACATTTTGACCATGGTGGGCAACCT
 GCTCATTTGTAGTGACCGTAACTGTCAGTGAGACCTGGGCTCACCAATGCTCTCTTCTTCT
 GCTGGCTTAACATTTATAGATATCATTATTTCTCATCCATTCCCCAGATTGATTTCAGA
 10 CTGTGTTCTTTGGGAATAATCCATATCCTTCCAATCTTTCATGGCCAGCTCTTATCGAGC
 ACCTTTTGGTGGGTCAGAGGTCTTTCTCTGTTGGTGATGGGCTATGACCGCTATGTGGC
 CATGTGTAAGCCCTTGCATTATTTGGTTATCATGAGACAAATGGGTGTGTTTGTCTGCTG
 GTAGTGCTCTGGGTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC
 TCCCATCTGTGGGCCCAATGTCATTGATCAITTTTCTGTGACATGTATCCCTATTGAAAT
 15 TGCCGCTGCAGTGACACCCATGTTATTGGCTCTTAAGTGGTGCCCAATGGAGGACTGCTCT
 GCACATTCAGCGTTTCTGCTCTTACTCATCTCTTATGGTGTCATCTCTGCACCTCTCAAGAA
 CTTAGTCAGAAAGGAGGCAAAAAGCCCACTCAACCTGCAGTTCACCATCACTGTGGGTTG
 TCTTCTCTTTGTTCTGTATTTTATGTGTGCTAGACCTGTAGGACCTTCTCCATTGAC
 20 AAATCAGTGAGTGTGTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC
 TGAGAAATCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

AOLFR22 sequences:

25 MRXXNXXTEFVLLGFSQDPGVXKALFVMFLTYXXTVVGNLLIVVDIIASPLXGSPMYFFLAC
 LSFIDAAYSTTKPIKLVGLFCDKKTISFGQCMGQLFDHFFGGAEVFLVVMACDRYVAICKPL
 30 HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPGFPGXVIVHFSKCDMHPHLELACTDTYFI
 GLTVVNVNSGAICMVIFNLLISYGVLSSSLKTYSQEKRKALKALSTCSSGSTVVVLFVFPICFIYVRP
 VSNPTDKFMTVFYTIITHMLSPLIYTLRNSMRNAIEKLGLKKLTIFIGGVSVLM (SEQ ID NO:
 43)

25 ATGAGACANNNNNAACAATATNACAGAATTGTCTCTCTGGGCTTTTCTCAGGATCTCGTGTG
 TGNNNAAAGCATTAATTGTGTCATGTTTTACTTCACATACNNNNNNNACAGGGTGGGGAACTCT
 GCTCATTTGNTGGGATATTAATGCCAGCCCTNNNTGGGTTCCCCAAGTATTTCTTCTCTG
 30 CCTGCTGTCATTATATAGATGCTGCATATTCACACTCAACTTTCTCCCAAGTAAATGTAGAGC
 TATTTCTGTGATAAAAAAGCATTTCTCTTCCAAGGTTGCATGGGCCAGCTATTTATAGAAC
 ATTTCTTTGGTGGGGCTGAGGTCTTCTCTGTTGGTGATGGGCTGTGATCGCTATGTGGC
 CATCTGTGAAGCCATGCACTATTTGACCATCATGAATCGACAGGTTTGTCTCTCTGTGTGG
 35 TNNTNNCCATGATTGGAGGTTTGTACATTCTGCGTTTCAAATTTGTTGTACAGATCTCCCT
 TCTGTGTGTCCTNATGTCATTGTTCAATTTTCAGTTGTGACATGCACCCATTAAGTGAACCTGGC
 ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTGTCAATAGTAGGCTACTCTGTATG
 40 GTCAATTTCAACCTTCTGTTAATCTCCTATGGAGTCATCTTAAGCTCCCTTAAACCTACAG
 TCAGGAAAAGAGGGGGTAAAGCCCTGTGTACCTGCAAGCTCCGGCAGTACCGTTGTGTCTCT
 TTTTTGTACCCCTGTATTTTCATATATGTTAGACCTGTTTCAAATCTTCTACTGATAAGTT
 CATGACTGTGTTTTATAACCATATACACACATGTGTGAGTCTTTAATATATACGTTGAGA
 AATTACAGATGAGAAATGCTATAGAAAAAATCTTGGGTAAAAAGTTAACTATATTTAATTA
 TAGGAGGAGTGTCCGTCTCATGTAG (SEQ ID NO: 44)

AOLFR23 sequences:

45 MAKNNLTRVTEFILMGFMDHPKLEIPLFLVLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS
 HLSLDDACYTSVITPQILATLATGKTVISYGHCAAQFFLTICAGTECFLLAVMAYDRIAIRNP
 LLYTVAMNPRLCWSLVVGYVCGVSGAILRTTCTFLSFCKDNQINFFCDLPPLLKLACSDTA
 NIEIVIFFGNFVILANASVILISYLLIILKTLKVKSSGGRKATFTSCASHITAVALLFFGALIFMYLQS
 GSGKSLIEDKVGVSFYTVVPIMLNPLIYSLRNKDVDFARKVARRIKQVLSLM (SEQ ID NO: 45)

50 ATGGCCAAGAAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC
 CCAAAATGGAGATTCCCTCTTTCTGGTGTCTTGAGTTCACCTAGTACACCTCTTGGG
 AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACCTACACCCCAATGTACTCTT
 TCTGAGCCACTCTCCCTGCTGGATGCGTGTACACCTCAGTCATCCAGCCCTCAGATCTTA
 55 GCCACATTTGGCCACAGGCAAAAACGGTCACTCTCTACGGCCACTGTGCTGCCAGTCTTTT
 TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGTAGGCTATGATCGCTA
 TGCTGCCATTTCGAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC
 CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTGAGGAGCATCTGCGTACCCTTGACACT

TCACCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCACCCCTGT
CTGAAGCTTGCTCGAGTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT
TTGTGATTTTGGCCAAATGCCTCCGTATCTCTGATTTCTATCTGCTCATCATCAAGACCATT
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAAGACTTTCTCCACATGTGCTCTCACATCA
5 CTGCTGTGGCCCTTTCTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAAGTGGCTCAGGCAAA
TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCAATCCCCATGCTGAACC
CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAGACGCCCTCAGAAAGGTGCTAGGA
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

10 **AOLFR25 sequences:**

METGNLTWVSDFVLGLSQTRELRFLFMLEFVYITTVMGNIITITVTSDSLHTPMYFLLRN
LAVLDLCFSSVTAPKMLVDLLSEKKTISYQCGMGQIFFHFLGGAMVFFLSVMAFDRLIAISRPL
RYVTVMNTQLWVGLVVAATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVRLACTDT
15 SLLEFLKISNSGLLDVVWFFLLMSYLFILVMLRSHPGEARRKAASTCTTHIVVSMIFVPSIYLY
ARPFPTFPMDKLVISIGHTVMTPLNPMIYTLRNQDMQAAVRRRLGRHRLV (SEQ ID NO: 47)

ATGGAACACAGGAACCTCACGTGGGTATCAGACTTGTCTTCTCGGGGCTCTCGCAGACTC
GGGAGCTCCAGCGTTTCTGTCTTAATGTCTCTGTTGTCTACATCACCCTGTTATGGGA
20 AACATCCTTATCATCATCAGTGACCTCTGATTCCAGCTCCACACACCCATGTACTTCT
GCTCCGAAACCTGGCTGTCTTAGACCTCTGTTTCTCTTCAGTCACTGCTCCAAAAATGCTAG
TGGACCTCTCTCTGAGAAGAAAAACCATCTCTTACCAGGGCTGCATGGGTACAGATCTTCT
CTTCCACTTTTGGGAGGTGCCATGGTCTTCTTCTCTCAGTGTATGGCCTTGACCGCCTCA
TTGCCATCTCCGGGCCCTCCGCTATGTCAACCTCATGAACACTCAGCTCTGGGTGGGGCT
25 GTGGTAGGCCACTGGGTGGGAGGCTTGTCCACTCTATTGTCCAGTGGCTCTGATGCTC
CACTGCCCTCTGTGGCCCAACATTTGGATAACTTCTACTGTGTATGTTCCCAAGTACT
GAGACTTGCCTGCACTGACACCTCACTGTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG
CTGGATGTCTGTCTGGTTCTTCTCTCTCTGATGTCTACTTATTCACCTGGGTGATGCTGAG
GTCACATCCAGGGGAGGCAAGAAAGGAAGGCAGCTTCCACCTGCACCAACCCACATCATCGT
30 GGTTCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATCCCTA
TGGACAAGCTGTGTGTCATCGGCCACACAGTCAACCCCATGCTCAACCCCATGATCTA
TACCTGAGGAACAGGACATGCAGGCAGCAGTGAAGAATTAGGGAGACACCGGCTGTT
TTGA (SEQ ID NO: 48)

AOLFR26 sequences:

MAAKNSSVTEFILEGLTHQPLRIPLFFLFLGFYTVTVVGNLGLTILGLNSHLHTPMYFFLNL
LIDFCSTTTHPKMLMSFVSRKNIISFTGCMTQLFFCFVVSFESILSAMAYDRYVAICNPLLYT
VTMSQVQLLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDIPLLEILSCNSSYMN
ELVVFIIVAVDVGMPHIVTIFISYALILSSILHNSSTEGRSKAFSTCSSHIIVSVLFFGSGAFMYLKP
40 LSILPLEQGVSSFLYTHIVPVLNPLIYSLRNKDKVALRRTLGRKIFS (SEQ ID NO: 49)

ATGGCAGCCAAAACTTCTCTGTGACAGAGTTATCTCTGAAGGCTTAACCCACCAGCGGG
GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTCTTACACGGTACCGTGGTGGGGAA
CCTGGGCTTGATAACCTGATTGGGTGAACCTCTCACCTGCACACTCCCATGTACTTCTCC
TTTITAACCTCTCTTAATAGATTCTGTTTCTCCACTACCATCACTCCAAAAATGCTGATG
45 AGTTTGTCTCAAGGAAGAACATCATTTCTTACAGGGTGTATGACTCAGCTCTTCTTCTT
CTGCTTCTTGTGCTCTCTGAGTCCTTCATCTGTGACGATGGCGTATGACCGCTACGTGG
CCATCTGAACCCACTGTTGTACACAGTCAACCATGCTTGGCAGGTGTGTTGCTCTCTTTG
TTGGGTGCTATGGGATGGGGTTTGTCTGGGGCCATGGCCACACAGGAAGCATATAATGAAC
CTGACCTTCTGTGCTGACAACTTGTCAATCATTTGATGTGTGACATCTTCTCTCTCTTGA
50 GCTCTCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTATTTGTGGTGGCTGTGAC
GTTGGAATGGCCATGTCACTGTCTTATTTCTTATGCCCTCACTCTCCAGCATCTTACACA
CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCACTGCCAGTCCCAACATAATTGTA

AOLFR27 sequences:

- MPSQNYSIIEFNLFGSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATIWIEHRLHTPMYFLFLCTL
SVSEILFTVAITPRMLADLLSHHSITFVACANQMFFSFMFGTHSFLLVMGYDRYVAICHPLR
5 YNVLMSPRDCAHLVACTWAGGSVMGMMVYTTIVFHLTFCGSNVHHFFCHVLSLLKLACENKT
SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKFTSCVSHLTVVTVHSFASFIY
LKPKGLHSMYSDALMATYTVTFPFLSPIIFSLRNLKLNAINKNFYRKFCPPSS (SEQ ID NO:
51)
- 10 ATGCCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTCCCC
CCAGCACCTCTCGCCCATCTGTCTCTGCTGTACCTCTGTGATGTTCTCTGTTACATTGCTGG
GCAACCTTCTCATCATAGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
CTTCTGTGTCACCTCTCCGTCTCTGAGATTCTGTTCACTGTGCCATCACCCCTCGCATGC
15 TGGCTGATCTGCTTCCACCCATCATTCATCACCTTTTGTGGCTGTGCCAACCAGATGTTCT
TCTCCTTCATGTTTGGCTTCACTCACTCCTTCTCTCTCTGGTCATGGGCTATGATGGCTA
TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCGTGACTGTGCCAT
CTTGTGGCCTGTACTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAAACGATAGTTT
TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTTTTCTGTCACTGTGCTTTCCCTCT
20 TGAAGTTGGCTGTGAAAACAAGACATCATCTGTCACTATGGGTGTGATGCTGGTGTGTGT
CAGAGCCTGATAGGCTGTTTATTCCTCATCCTCTCTCATGTCTTCACTGTGGCTGCCA
TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTTTCTACGTGTGTATCCACCT
CACTGTGGTGGTCAAGCACTATAGTTTGTCTCCTTTATCTACCTCAAGCCCCAAGGGCCTCC
ATTCTGTACAGTGAAGCCTTGATGGCCACCACCTATCTGCTTCAAGCCCTCTCTTAGC
25 CCAATCATTTTCAAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAAATAAACTTTTACA
GAAAATTCTGTCTCCAAGTCTCTGA (SEQ ID NO: 52)

AOLFR28 sequences:

- MPNFRTDTEFTLLGLTCRQELQVLFVVFLAVYMITLLGNIGMILLISIPOLQSPMYFFLSHLSF
ADVCFSSNVTPKMLENLLSETKTISYVGLVQCYFFIAVHVHVEVYILAVMAFDYRMAGCXPLL
30 YGSKMSRVTVCRLISXYXYGFSVSLICTLWTYGLYFCGNFEINHFYCADPPLQIACGRVHIKE
ITMIVAGINFTYSLSVLISYTLIVVAVLRMRSDAGRRKAFSTCGSHLTAVMFYGTPIFMYLRL
RPTESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKAVNKAITKTVVRQ (SEQ ID NO: 53)
- 35 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCTGGGGCTGACCTGTCGTGAGGAGC
TACAGGTTCTCTTTTTGTGGTGTCTCTAGCGGTTTACATGATCACTCTGTTGGGAAATATT
GGTATGATCATTTTGATTAGCATCAGTCCTCAGCTTCAGAGTCCCATGTACTTTTCTCTGAG
TCATCTGTCTTTTGGCGACGTGTGCTTCTCTCCAAACGTTACCCCCAAAATGCTGGAAAACCT
TATTATCAGAGACAAAACCATTTCTATGTGGGATGCTTGGTGACGTGCTACTTTTTCAT
40 TGCCGTTGTCCACGTGGAGGCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC
GGCTGCAANCCCTGTCTTTATGGCAGTAAAAATGTCTAGGACTGTGTGTGTCGGCTCATCT
CTGTGNNNTATGNNATGGATTCTCTGTGACCTAAATATGCACACTATGGACTTATGGCTT
ATACCTCTGTGAAAACCTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA
TGCTCTGTGGGAGAGTGCACATCAAAGAAATCAAAATGATTGTTATGTCTGGAATTAACCT
45 CACATATTCCTCTCGGTGGTCTCATCTCTCTACACTCTCATTGTAGTAGCTGTGCTACGCA
TGCGCTCTGCGGATGGCAGGAGGAAGGCGTTCTCCACCTGTGGGTCCCACTTGACGGCTGT
TTCTATGTTTTATGGGACCCCCATCTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA
GAGCAGGGCAAAATGGTGGCTGTGTTTACACCACAGTAATTCCTATGTGTGAATCCCATGA
TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCAACGAAGCAT
50 ATGTGAGGCAGTAA (SEQ ID NO: 54)

AOLFR29 sequences:

- MMSFAPNASHSPVFLVLLGFSRANISYTLFFFLAIYLLTILGNVTLVLLISWDSRLHSPMYLLRL
GLSDVMGLSTVTLPLQLLAHLVSHYPTIPARCLAQFFFFYAFGVTDTLVIAVMALDRYVAICD
PLHYALVMNHQRCACLLALSVVVSILHTMLRVGLVPLPCWTGDAGGNVNLPHFCDHRPLLR
55 ASCSDIHSNELAIFFEGLMLGPCALIVLSYVRIGAAAILRIPSAAGRRRAVSTCGSHLTMVGFLL

ATGATGAGCTTTGCCCTAATGCTTCACACTCTCCGGTTTTTTTGTCTCTGGGTTCTCGAG
5 AGCTAACATCTCTACACTCTCTCTTCTCTGTCTGGCTATTACCTGACCACCATAC
TGGGGAATGTGACACTGGTGTCTGCTCATCTCTGGGACTCCAGACTGCACCTACCCATGTA
TTATCTGCTTCTGTGGCTCTCTGTGATAGACATGGGGCTATCCAGACTTACACTGCCCCAG
TTGCTGGCCCAATTGGTCTCTCAATTACCAACCATCTCTGCTGCCGCTGCTTGGCTCAGTT
10 CTTTTCTTCTATGCATTGGGGTTACAGATACACTTGTCAATTGCTGTCACTGGCTTGGATC
GCTATGTGGCCATCTGTGACCCCTGCACATGCTTTGGTAATGAATCACCACCGGTGTGC
CTGCTTACTAGCCTTGAGCTGGGTGTGTCCATACTGCACACCATGTGCGTGTGGGACTC
GTCTCGCTCTTTGTCTGGACTGGGGATGTGCGGGCAACGTTAACTTCTCACTCTTTTTG
TGACCAACCGGCCACTCTGCGAGCCTCTGTCTGACATACATTCTAATGAGCTGGCCATA
TTCTTTGAGGGTGGCTTCTTATGTCTGGGCCCTGTGCCCTCAITGTACTCTCTATGTCCG
15 AATTGGGGGCTGATCTACGTTTGCCTTCAGCTGCTGGTCCGCCGCGAGCAGCTCCACC
TGTGGATCCCACTCACCATGGTGGTTTCTCTACGGCACCATCATTTGTGTCTACTTCCA
GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTCAGTAATGTATACTGCCATT
ACACCTTTGGCCCAACCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCACCTC
GCAGGCTGCTTGAATGGGTGAAGGTAGACCCTGA (SEQ ID NO: 56)

20
AOLFR30 sequences:
MGFLSPMHPCRPPTQRRMAAGNHSTVTEFILKGLTKRADLQLPFLFLGYYLVTVGNLGMIT
LCLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNIIISYAGCMSQLYFLVFLVIAEC
YMLTVMAYDRYVXXCHPLLYNIMSHHTCLLLAVVYAIGLGSTIETGLMLKLPYCEHLISHY
25 FCDILPLMKLSCSSTYDVEMTVFFSAGFNHVTSLTVLSYTFILSSILGISTTEGRSKAFSTSSSHL
AAVGMFYGSTAFMYLKPTSISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAQVQKTLRGK
LF (SEQ ID NO: 57)

ATGGGGTCTTGCTCTCCCATGCATCCCTGCGAGCCTCCCACCCAGAGGAGAATGGCTGCAG
30 GAAATCACTCTACAGTGACAGAGTTCATTCTCAAGGGTTTAAACGAAGAGAGCAGACTCC
AGTCCGCCCTTCTTCTCTCTCTCGGGATCTACTTGGTCAACCTCCGCGGGAACCTGGGC
ATGATCACTCTAATTGTCTGAACCTCAGCTGCACACCCCATGTACTACTTCTCAGCAA
TCTGTCACTCATGGATCTCTGCTACTCCTCCGTCATTACCCCTAAGATGCTGGTGAACATTG
35 TGTCAGAGAAAAACATCATCTCTACGCGAGGTGCATGTCAAGCTCTACTTCTCTCTGT
TTTTGCTATTGTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCTC
TGCCACCCCTTGCTTTACAACATCATTTATGTCTCATCACCTGCTGCTGCTGGTGGCTGT
GGCTACGCCATCGGACTCATTTGGCTCCACAATGAACACTGGCCTCATGTTAAACTGCC
TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACACTCTCCCTCTCATGAAGCTGTCTGT
CTTAGCACCTATGATGTTGAGATGACAGTCTCTTTTCGGGTGGAATTCACATCATAGTC
40 ACAGGCTTAAACAGTTCTTGTTCTTACACCTCAITCTCTCAGACATCTCCGGCATCAGAC
CACAGAGGGGAGATCCAAAGCCTTACGACCTGCAGCTCCCACTTGACGCGTGGGAAT
GTTCTATGGATCAACTGATTCATGTACTTAAACCCCTCCACAATCAGTTCCTTGACCCAG
GAGAATGTGGCTCTGTGTTTACACCAACGTAATCCCATGTTGAATCCCTCAATCTACA
45 GCCTGAGGAACAAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTT
GA (SEQ ID NO: 58)

AOLFR31 sequences:
MGTGNDTIVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISHIIVIRRRSHLHTPMYIFLCHL
AFVDIYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAEFLAAMAYDRYVAICSP
50 LLYSTCMSPGVCIILVGMSSYLGCCVNAWTFIGCLRLSFCGPNKVNHHFFCDYSPLLKLACHSHDF
TFEIIIPAISGSIIVATVCVIAISYIYLITILKMHSTKGRHKAFSTCTSHLTAVTLFYGTITFIYVMP
KSSYSTDQNKVVSVFYTVVIMPLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA
55 CTACAGTTTGTGCTATTTTATTTCTGTGTTTCTAGGAATTTATGTGCACCTTAATGGGT
AATATCAGACATAATTGATTGATCAGAGAAGTCACTCATCTCATACACCATGTACATTT

TCCTCTGCCATTGGCCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGGTC
ATGAGCTTCTCAAGGAAAGAAACCTCTCCCTGTGTGGTGGTGTGGCCAGCTGTGT
CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTCGTGGCTGCCATGGCCATGATGCGGTA
5 TGTGGCCATCTGCTCACCCTGCTCTACTCTACCTGCATGTGCCCTGGAGTCTGCATCAT
TAGTGGGCATGTCTACTCTGGGTGGATGTGTGAATGCTTGGACATTCATTTGGCTGCTTATT
AAGACTGTCTCTGTGGGCCAAATAAAGTCAATCACTTTTCTGTGACTATTCACGACTTT
TGAAGCTTGCTTGTTCOCATGATTACTTTTGAATAATTCAGCATCTCTCTTCTGGATCT
ATCATTTGTGGCCACTGTGTGTGCATAGCCATATCCTACATCTATATCCTCATACCATCTCT
10 GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCCTTCTCCACTGCACTCCCACTCACT
GCAGTCACTCTGTCTTATGGGACCATTACCTTCATTATGTGATGCCCAAGTCCAGCTACTC
AAGTACCAGAACCAAGGTGGTGTCTGTGTCTACACCGTGGTGATTCCCATGTTGAACCC
CTGATCTACAGCCTCAGGAACCAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
AAAATATTTTCTTGA (SEQ ID NO: 60)

15 **AOLFR32 sequences:**

MNSLKDGNHTALTGFILLGLTDDPILRVILFMILSGNLSIILIRISSQLHHPMYFFLSHLAFADM
AYSSSVPMNMLVNLVERNVSYLGCALQLSAAFFATVECVLLAAMAYDRFVAICPLLSTYTK
MSTQVSPVQLLVVYAGFLIAVSYYTTFYFLFCFQPNQVNHFFCDLAMELRLSCDISVSVTVLSF
SSGSHIVTVVCVIAVCYIYILITILKMRSTEGHHKAFSTCTSHLTVVTVLFYGTITFIYVMPNFSYST
20 DQNKVVSVLVTVVPMPLNLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID
NO: 61)

ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCTATTGGGCTTAA
CAGATGATCCAACTCTGAGTCATCTCTTCATGATCATCTATCTGGTAATCTCAGCATA
25 ATTATCTTATCAGAATTTCTTTCAGCTCCATCATCTATGTATTCTTTCTGAGCCACTT
GGCTTTTGTGACATGGCCTATTCACTTCTGTGCACACCAACACTGCTTGTAACTCTCTCG
TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGTGTACGGCGCTTCTT
TGCAACAGTCGAATGCCTCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC
AGTCCACTGCTTTATTCACCAAAAAATGCCACACAAGTCAAGTCCAGCTACTCTTAGTAG
30 TTTACATAGCTGGTTTCTCATTTGCTGTCTCCTATACTACTCTCTTCTATTTTACTCTCT
GTGGACCAAAATCAAGTCAATCATTTTTTCTGTGATTTTCGCTCCCTACTTGAAGTCTCTGT
TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTCTCTGGATCCATCATTTGTGGTCA
TGTGTGTGTATAGCCGTCTGCTACATCTATATCCTCATCACCATCTGAAGATGCGGTCCA
35 CTGAGGGGACACCAAGGCCCTTCTCCACTGCATCTCCCACTCACTGTGGTACCTCTTCT
CTATGGGACCATTAACCTTCATTTATGTGATGCCCAATTTAGCTACTCAACTGACCAGAAC
AAGGTGGTGTCTGTGTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
TCAGGAACCAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTGTTAGAAAAATACCTTTCTC
ATGATGCTTGTATTATTTAGTAGAAGCTTCAATAATGATATTACATAG (SEQ ID NO: 62)

40 **AOLFR34 sequences:**

MLEGVEHLLLLLLTDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVIYLLTVSGNG
LILITVLVDIRLHRPMLCLFLCHLSFLDMTISCAIVPKMLAGFLLSRISFSGCVQLFSFHGLCT
ECFLYTLMAYDRGFIACGLPHYATIMTHRVNCSLALGTWLGTHLSLFTQSFVRLPCFQPNRV
DYFCDIPAMLRLACADTAINELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRRNAFST
45 CAHLTVVIVVYVPCFTFIYLRPCSQEPLDGVVAVFYTVITPLNLSIHYTLCKNEMKAALQRLGG
HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTGAGCATCTCCTTCTGCTACTCTTTTGACAGATGTGAACAGCAAGG
AACTGCAAGTGGAAACAGACTTCTGTGTCTCACTTCATTTTGGTGGGCTGCACCAACCC
50 ACCACAGCTGGGAGGCCACTCTTCTAGCTTCTGTGATCTATCTCACTCTCACTGTTTCTG
GAAATGGGCTCATCATCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCATGTGCTT
GTTCTGTGTCACTCTCTCTTCTGGACATGACCAATTTCTGTGCTATGTGCCCAAGATGC
TGCTGGCTTTCTCTGGGTAGTAGGATATCTCTTCTGGGGCTGTGTAATCCAATATT
TCTTTCCATTTCTGGGCTGTACTGAGTGCTTCTTACACACTCATGGCTATGAGCGTTT
55 TCTTGCCAATTGTAAGCCCTACACTATGCTACCATGACCCACAGGCTCTGTAACCTCC
TGGCTTAGGCACCTGGCTGGGAGGACTATCAATCACTTTTCCAACAAGTTTGTATT

TGTGGTTGAGAAAGGGCAACCACATTCATCCCTACATCTGCAAACTCTGCCCTTAG
(SEQ ID NO: 68)

AOLFR37 sequences:

- 5 MEKANETSPVMGVLLRLSAHPELEKTFVVLILLMYLVILLNGVLLVLTILDSRLHTPMYFFLG
NLSFLDKICTSSVPLVDLSFLTQETISFSAACVQMAISFAMAGTECLLSMMAFDRYVAICNP
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVFLGVPVLFISFVFIITILRPSAEGRRKVFSTCSAHLTVVIVFYGLFFMYG
10 KPKSKDSMGADKEDLSDKLIPFYGVVTPMLNPIIYSLRNKDVKAAVRRLLRPKGFTQ (SEQ ID
NO: 69)

- ATGGAAGAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACTCGTGATCCTGCT
GGCAATGGGGTCTCATCTCTGGTGACCATCTCTGACTCCGCGCTGCACACGCCCATGTAC
15 TTCTTCTAGGGAACCTCTCCTCTGGACATCTGCTCACTACCTCTCAGTCCCACTGGT
CTGGACAGCTCTTTTGACTCCCAAGAAACCATCTCCTTCTCAGCTGCTGTGCGAGATG
GCACTCTCCTTTGCCATGGCAGGAACAGAGTGTCTTGCTCCTGAGCATGATGGCATTTGATC
CTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
GCCCATGGCTGCCAGCTCTGGGCTATTGGTGGTGCTGCTCCGTGGTACACACATCCTTG
20 GCAATTCAAGTCCCTCTCTGTTGGAGACAATGATCAACCACTTCACTGTGAGATCTTGG
CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTATCAGCATGGAGGTTGACGAA
TGTGATCTTCTAGGAGTCCCGGTTCTGTTCACTCTCTTCTCCTATGTCTTCATCATCACCA
CCATCTGAGGATCCCTCAGCTGAGGGGAGGAAAAGGTTCTTCCACCTGCTCTGCCCA
CTCACCGTGGTGATCGTCTTCTACGGGACCTTATCTTCAATGATGGGAAGGCTAAGTCT
25 AAGGACTCCATGGGAGCAGACAAGAGGATCTTTCAGACAACTCATCCCCCTTTCTATG
GGTGGTGACCCGATGCTCAACCCATCATCTATAGCTGAGGAACAAGGATGTGAAGG
CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

- 30 MYLVTVLRNLLILAVSSDHLHTPMCFLLSNLCWADIGFTSAMVPKMIVDMQSHSRVISYAGC
LTQMSEFFVLFACIEDMLLTVMAYDRFVAICHPLHYPMVNPHLGVFLVVSFFLSLLDQLHSW
IVLQFTFFKNVEISNFCVDPQLLNLCSDSVINSIFIYLDSIMFGFLPISGILLSYANNVPSILRISS
SDRKSAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPPRNGVVASVMYAVVTPMLNPIIYSLR
NRDIQSALWRLRSRTVESHDLSSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

- 35 ATGTACTGGTACCGTGTGAGGAACCTGCTCATCATCTGGCTGTGAGCTCTGACTCCC
ACCTCCACACCCCATGTGCTTCTTCTCTCCAACTGTGCTGGGCTGACATCGGTTTCCAC
TCGGCCATGGTTCCCAAGATGATTGTGGACATGCACTGCGATAGCAGATCATCTCTTATG
CGGGCTGCCTGACACAGATGTCTTCTTTGCTCTTTTTCATGTATAGAAGACATGCTCCTG
40 ACAGTATGAGGCTATGACCGATTGTGGCCATCTGTCAACCCCTGCACTACCCAGTCATCA
TGAATCTTCACCTGGTGTCTTCTTAGTTTGGTGCTCTTTTCTCAGCTGTGGATTTCC
CAGCTGCACAGTTGGAATTGTGTACAATTCACTTCTCAAGAATTGGGAAATCTCCAATT
TTGTCTGTGACCATCTCAACTTCTCAACCTTGCTGTTCTGACAGTGTATCAATGACAT
TTCATATATTTAGATAGTATTATGTTGGTTTCTTCCCATTTCAAGGATCTCTTGTCTTAC
45 GCTAACAAATGTCCCTCCATTCAAGAATTTCAATCATCAGATAGGAAGTCTAAAGCTTCT
CCACCTGIGGCTCTACCTGGCAGTTGTTTGTCTATTTATGGAACAGGCATTGGCGTGTA
CTGACTCTCAGCTGTGTCAACCCCCCAGGAATGGTGTGGTGGCATCAGTGAATGATACGT
GTGGTCAACCCCATGCTGAACCCCTTTCATCTACAGCTGAGAAATAGGACATCAAGAGTG
CCCTGTGGAGGCTGCAGCAGAACAGTGAATCTCATGATCTGTTATCTCAAGATCTGCT
50 CCATCTGTTTCTTGTGTGGTGAGAAAGGTCAACCCATTA (SEQ ID NO: 72)

AOLFR39 sequences:

- MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIRLNRLHTPMYFFLSS
LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMQLFFFCVVCVISECYMLAAMACDRYVAICSPL
55 LYRVIMSPRVCSLLVAAVFSVGTDAVHGGCILRLSFCGNSIIKHYPFDIVPLIKLSCSSYIDEL

LIFVIGGFNMVATSLTHIISYAFILTSILRIHSSKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS
SSSLTQEKVSSVFYTTIVILMLNPLIYSLRNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)

5 ATGGGTGTAAAAACCATTCACAGTGACTGAGTTTCTTCTTTCAGGATTAAGTGAACAA
CAGAGCTTCAGCTGCCCTCTTCTGCCCTCTTCTAGGAATTAACAGGTTACTGTGGTGGG
AAACGATCAGCATGCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTACTAT
TTCTGTAGTAGTTTGTCTTTTATAGATTCTGCTATTCTTGTGCAATACCCCTAAAAATGCT
ATCAGGGTTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTCAAGCTGTTT
10 TTTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGGCATCGCTAC
GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCCTAGGGTCTGTTCTGTC
TGGTGGCTGCTGCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTGTATACT
CAGGTTGTCTTTCTGTGGATCAAAATCATTAACACATTATTCTGTGACATTGTCCCTTTA
TTAAACTCTCTGCTCCAGCACTTATATIGATGAGCTTTTGATTTTGTCAATTGGTGGATT
AACATGGTGGCCACAAGCCTAACATCATTATTTCATATGCTTTTATCCTCACCAGCATCT
15 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGCCACCTGCAGCA
GCTGTTCTTATGTTTTATGGGTCTCTGATGTCATGTATCTCAAACCTGCTCTAGCAGTTC
ACTCACCCAGGAGAAAGTATCCTCAGTATTTTATACCAGTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

20
AOLFR40 sequences:

MSDNALLTAFILTGPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFTSVTVPKMLMTLVSPSGRTISFHSVQALYFFHFLGSTECFLYTVMSYDRYLAISYPL
RYTNMMTGRSCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTS
25 ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSLRIRTSEGRHRAFCASHCIVLFCFGPGLFIYL
RPGSRDALHGVVAVFYTTLTPLFNPVVYTLRNEVKKALLKLKNGSVFAQGE (SEQ ID NO:
75)

30 ATGTCCAACGCCACCCCTACTGACAGCGTTTCACTCTCACGGGCGCTTCCCCATGCCCAAGGGC
TGGACGCGCCCTCTTGGAAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CTTCATCTCTGCTGGTATCAGGGTGGATTCTCACCTCCACACCCCATGCTACTTCTCTCA
CCAACTCTGCTTCAITGACATGTGGTTCTCCACTGTGACGGTGCCCAAAATGCTGATGAC
CTTGCTGTCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTGCTGCTATATTTT
35 TCCACTCTCTGGGAGCACCAGAGTGTCTCTACACAGTCATGTCTATGATCGCTACTCT
GGCCATCAGTTACCCGCTCAGGTACACCAACATGATGACTGGGCGCTGCTGTGCCCTCTG
GCCACCGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATGCACTTCC
ATTTCGCCATCTGTGGACCAACAGATCCAGCACTACTCTGTGACGCACGCCCATCCT
GAAACTGCTGTGCAGACACCTCAGCCAAACGAGATGGTCACTCTTGTGAATATTGGGCTA
40 GTGGCTCTGGGCTGCTTTGCTGATAGTGCTGTCCTATGTGTCATCGTGTGTTCCATCT
CGGATACCGCACTCAGAGGGGAGGCACAGAGCTTCCAGACCTGTGCCCTCCCACTGTATC
GTGGTCTTTGCTTCTTGGCCCTGGTCTTTTCATTACCTGAGGCCAGGCTCCAGGGGACGC
CTTGATGGGGTGTGGCCGTTTCTACACACGCTCACTCTCTTTCAACCTGTTGTGTG
ACACCCTGAGAAACAAGGAGGTAAGAAAGCTCTGTGAAGCTGAAAAATGGGTCAAGTAT
45 TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

AOLFR41 sequences:

50 MNPENWTQVTSFVLGFPSSHLIQFLVFLGLMVTYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLVTVVVKMLLVILTGDHTISFVSCIQSYLYFFLGTDDFFLLAVMSLDRLYLAICRPLR
YETLMNGHVCSQVLVASWLAGFLWLCPVTLMASLPFCGPNIGDHFDRDSWPLLRLSCGDTH
LLKLVAFMLSTLVLLGSLTSVSYACILATVLRAPTAERRKAFSTCASHLTVVVIHGGSSIFLY
IRMSEAQSKLLNKGASVLSCHITPLNPFITLRNDKVQQAALREALGWPRLTAVMKLRVTSQRK
(SEQ ID NO: 77)

55 ATGAACCTGAAAACTGGACTCAGGTAACAAGCTTTGTCTTCTGGGTTTCCCCAGTAGCC
ACCTCATACAGTTCTGGTGTCTCTGGGGTTAATGGTGACCTACGTATGAACAGCCACAGG
CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACCGCTGCATCATACAGATGACTTCT

GGGGTTTGATTCTCTCTCCCACTGCCCTTCATCCTCAAGTGGTGTGCTACTGCCAAACAC
 ATACTGTCAACACACTCCTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC
 CAGGTGCAATGTGGTTTATTGGAAGCTCTTCATCATCCTCTCAGTCATGGGTGTGGAGCTCTCTCT
 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTGTGGAGCTGTCTCTCGGAGGGCA
 GCACTCGAAGGCTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTCTATGTACC
 CCTCATTTGGGCTCTCGGTGTGCATAGGCTGGGTGGTCCCACCTCCTCCTCCATGTGGTT
 ATGGCTAATACCTACTTGTGCTACCACTGTAGTCAACCCCTTGTCTATGTGGAGCGAAGA
 CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAAGTGGCAAGTGA (SEQ ID
 NO: 82)

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFVWGFLLSMYVVMFGNCIVVIVRTERSLHAPMYLFLC
 MLAAIDLALSTMPKILALFWFDSREISFEACLTQMFHIALSAIESTILLAMAFDRYVAICHPL
 RHAAVLNNVTVAQIGIVAVVRGSLFFFLPLLKRLAFCHSNVLSHSYCVHQDVMKLAYADVGLP
 NVVYGLTALLVMGVDVMFISLYFLIIRTVLQLPSKSERAKAFGTCVSHIGVLAFFYVPLGLS
 VVHRFGNSLHPIVRVVMGDIYLLPPVINPIHYGAKTKQIRTRVLMAMFKISCDKDLQAVGGK
 (SEQ ID NO: 83)

ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCAGGATTAGAGA
 AAGCCCATTTCTGGGTGGCTTCCCCCTCCTTCCATGTATGTAGTGCAATGTTTGGAAAC
 TGCATCGTGGTCTTCATCGTAAGGACGGAACGACGCTGCACGCTCCGATGTACCTCTTTC
 TCTGCAGCTTGCAGCACTTGACCTGGCCTTATCCACATCCACCAAGCTTAAGATCCTTGCC
 CTTTCTGTTTGGATTCCCGAGAGATAAGCTTGGAGCCTGTCTTACCCAGATGTCTTTAT
 TCATGCCCTCTCAGCCATTGAATCCACCATCCTGTCTGGCCATGGCCTTTGACCGTTATGTGG
 CCATCGCCACCCACTGCGCCATGCTGCAGTGCTCAACAATACAGTAACAGCCAGATTGG
 CATCGTGGCTGTGTGCCGGATCCCTCTTTTTTCCCACTGCCTCTGTGTATCAAGCGGC
 TGGCTCTTGCACCTCCAATGTCTCTCGCACTCCTATTGTGTCCACAGGATGTAAATGAA
 TGTGGCCTATGCAGACACTTGCCTAATGTGGTATATGGTCTTACTGCCATTCTGTGGTTC
 ATGGGCGTGGACGTAATGTTATCTCCTTGTCTATTTTGTGATAATACGAAACGGTCTGCA
 AACTGCCTTCCAAGTCAGAGCGGGGCCAAGGCCCTTGGAAACCTGTGTGTACACATTGGTGT
 GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAAACAGC
 CTTCATCCCAATTGTGCGTGTGTGCATGGGTGACATCTACCTGTCTGCTCCTGTGCATCAA
 TCCCATCATCTATGGTGCCAAAACCAACAGATCAGAACAGGGGTGCTGGCTATGTTCAAG
 ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

AOLFR45 sequences:

MLPSNITSTHPAVFLLVIGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIHQADAALHEPMYFLA
 MLATIDLVSSTTLPMKILAFWFRDQENFFACLQMPFLHSFSIMESAVLLAMAFDRYVAICKP
 LHYTTVLGTSLIKIGMAA VARAVLMTPLPFLRRFHYCRGPVIAHCYCEHHAVVRLACGDT
 SFNNIYGIAMAFSVYLDLLFVILSYVFLQAVLQASQEARYKAFGTCVSHIGAILSTYPPVIS
 SYMHRVARHAAAPRVHILLAIFFYLLFPPMVNPIIYGVKTKQIREYVLSLQFQKNM (SEQ ID NO:
 85)

TGGAAACAAGAGGTAACTTTGCAGGTGGGATAGCACAGGTGAACTCTAATCATATATA
 CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAAATTGCACAGGAGATTTCGA
 GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTGTGGTAGGAAT
 TCTGTGTTTGGAAACCTGCATGCCTGGATCTCCATCCCTTCTGCTTGTCTTACTACTCG
 CCTGTATGGAACCTGTATCCCTTCTCTTCAATTACAGGCTGATGACGCGCTCCATGAACCC
 ATGTACCTCTTCTGGCCATGTTGGCAACCAATTGACTTGGTCTTCTTCTTCAACACGCTGCC
 CAAAATGCTTGATATTTCTGGTTACGGGATCAGGAGATCAACTCTTTGGCTGTCTGGTC
 CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGTCTGTGGCCTATGGCCTT
 TGACCGCTATGGCCATCTGCAAGCCAATTGCCTACACAGCGTCTGACTGGGTCCTCCTC
 ATCACAAGATTGGCATGGCTGTGTGGCCCGGGCTGTGACACTAATGACTCACTCCCTCT
 TCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCATTGCTACTGTGAACA
 CATGGCTGTGGTAAGGCTGGCGTGTGGGACACTAGCTTCAACAAATATCTATGGCATGTCT
 GTGGCCATGTTTATGTTGGTGTGGAACTGCTCTTGTATCTGTCTTATGTCTCATCT

TCAGGCAGTTGTCCTCAGCTTGCCCTTCAGGAGGCCCGCTCAACAAAGCTATTGGGCATGTGTGT
TCTCATAAGTGGCCATCTGTCACCTACCTACGATAGTCACTCTCTCAGTACATGCACGC
TGTAGCCCGCCATGCTGCCCTCGTGTCCACATACTCTTGCTATTTTCTATCTCTTTCT
5 CAGCTATTCTTCAGAGAAAGCAATGTAGTAGTGTAGTGTCTTTTATCCCATCTGCCA
AGTAAATGAGAAATCTGGATTTGGGTTGAGGGGGAAAAAATCTAAATAGGAAAAATTCGACAGT
ATCTTTGACAATTTCTCATGTAGTAGTAAGGAAAAATGAGGTTTCACTTCTCCACAGATACAGA
GTACAGTTGACACAGGAGTGCACCTATAGTGTGCTGATAGTAGAGGTTTGACCTTCCCA
TTGTCTAGACTACATACATGCGCTAAGGAAGACAAACTCTCAAGTGTGGTATTTGTAATCTG
10 GGTGAAGACAGTAGGACCTTTATTTGGCTGAGATTGGCCCAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

MNLIKHCWGHMMHTWLNRREDDSDFCNFQIQGQISGNFHSITSRMYFLCFCSTLLGFKVHWVS
 SRLIXLKMLSPSPNDNSTAPVSEFLCLFVFNQFSQWQLWSLPLSLLLFLLMAGNTLLITIQLEAS
 LHQPLYYLLSLLDLVLCLTVPKVLFAIFWDLRISFSFACFLFMQFMNSFLTMESTCFMVMAS
 YDRYVAICHPLQYPSHIITDQFVARVGVFVIARNAFVSLPVPMLSARLYCAGNIUKCISNLSYLS
 LKSCDDITENLRYFSAHTGALLGSDLLILVIVSYFYLKAEKGAVALAKTSCGSHFLILFVS
 TVLLVLVTITNLARKRIPPDPVILLNLHLHLLPALNPVIVGVRTKEIKGQIQNLKRL (SEQ ID NO:
 87)

TGTGAATAATAAAACATTGTGGCTGGCATATGATACATACATGGTGTAAAATATAAGGGAGGAT
 GATGACAGTGATTTTAAAAACCTTATTGGACAGATACAGGCTTCATCGTGGAAACCCACAT
 CTACTACGTTCTAGAATGGTTTATTTATGTTCTGTGATCTTCTACTAGGTTTAAAGGTACAC
 TGGGCTTCCAGATGGATCANGAAACCTTACATGGCATCTCCCAACATGACTCATCTGCC
 CAGTCTCTGAATTCCTCTCATCTGCTTCCCAACTTCCAGAGTCTGGCAGCACATGGTTGTCT
 TCTGCCCTCAGGCTTCTCTCTCTCTGGCATGGGAGTACACCAACCCCTCTGATACCAT
 CCAGCTGGAGGGCTTCTGCGACAGCCGCTGTACTACTCTGCTCAGCCTCTCTCTCTGGTGG
 ACATCGTCTGTCTGCTCACCCTGATCCCCAAGGTCTGGCCATCTTCTGGTTTGACCTCAGG
 TCGATCATGCTTCCAGCCTGCTTCTCCAGGTGTTCATCATGAACAGTGTTTTGACATGGG
 TCTCGACAGTTATGGTTCATGGCTATACCGCTTATGTGGCCATCTGGCATCCATATGGA
 TACCGGCTCATCATCACTGACCAGTTTGTGGCTAGGGCGTGGTCTTGTGTATAGCCCGGA
 ATGCTTTTGTCTTCTCTCTTCCATGCTTCTGCCAGGCTCAGATATGCTGTGCAGGAAC
 ATAACTAAGAAAGTGCATCTGCAGTAAGCTGTCTGTGTTCCAACTCTCTGTGATGACATCT
 CTITTCACATCAAGCTCACCAGTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTATCTCT
 ATGTGATCTCTCTATCTTTATATTTAAGATTTGTGCTTAGGATCAAGGCCAGGGGTGCTG
 TGGCAGGCTCTGAGACATGCTGTGTTCCCATCTATCTCATCTCTCTCTCAGCACAGTCC
 TGCTGTTCTGTGTCACTCACTAACTGGCCAGGAAGAATCTCCAGATCTGTCCTCATCT
 CTCTCAACATCTGTCAACCACTCATCTCCCAAGCTCTGAACCCGTTGTATTTATGGTGTGGA
 ACCAAGGAGATCAAGCAGGGAATCCAAACCTGCTGAAGAGGTTTGAAT (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNTLTHPTAFLVLGPIGLEHLHIWISIPFLAYLTALLGNCTLLLIQADAALHEPMYLFLA
MLAALDVLSSSLPKMLAIFVARDREINFACLAGMFFHIFSGSIMEA VLLAMAFVAVAIK
PLHYTKVLGTSLITKIGMAAVFARVDTLMTPLFLRCHVYCRGPFVAHCHCEMAFVRLACD
TSFNNIYGIAMVAMFIVVLDLLLVLSYIFILQAVLLASQEARYKAFGTCVSHIGAILAFYTTVVIS
SMVMHVARHAAPHVHLIANFYLLFPMPVNPPIHGVKTKQIRESLGVFPRKDM (SEQ ID NO:
89)

ATGTTCAGCCTCCAATATCACTTAAACATCCAACTGCCTCTCTGTTGGTGGGGGATCCGAGCTCGTGAACACCTGCACATCTGGATCTCCATCCCTCTCTGCTAGCATATACATGGCCCTGTCTGGAAACCTGCATCTCTCTTCATCATCCGAGCGGTGATGAGCCCTCATGAAACCATGTACCTCTTCTTGGCCCATGTGGCAGGCATCGACCTGGTCTTCTTCCCTCAGCATGGCCAAAATGCTTGGCAATCTCTGGTTCAGGATTCGGGAGATAAATCTTCTGGCTGTCTGGCCAAAATCTTCTCTTCATCTCTCTTCATCATGGAGTCAGCAAGTGCTCTGGCCATGGCCCTTGACCGCTATGGGGCTATCTGCAAGGCACTGCATACCAAAGTGCTGACTGGGTGGCTCATCT

5 CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCCTCTCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGGTGG
CCATGTTTATTGGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATCTTTCAG
GCAAGTCTACTGCTTCCCTCTCAGGAGGCCGCTACAAGCAATTGGGACATGTGCTCTC
ATATAGGTGCCATCTTAGCCTTCTACACAACCTGTGGTCATCTCTCAGTCATGCACCGGTGA
GCCCGCATGCTGCCCTCATGTCCACATCTCCTTGCCAATTTCTATCTGCTCTCCCAACC
CATGGTCAATCCCAATAATCTATGGTGTCAAGACCAAGCAAAATCCGTGAGAGCATCTTGGGA
GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

10

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL
CMLSGDILISTSSMPKMLAIFWFSNTTIQFDACLLQMFIAHLSGMESTVLLAMAFDRYVAICH
PLRHATVLTLPVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMLKALCDDI
15 RVNVVGTGLIVHISAGLDSLLISFSYLLILKTVLGLTREAAQKAFGTCVSHVCAVFIFYVPFGLSM
VHRFSKRDSPLPVILANIYLLVPPVLNPVYGVKTKAIRQLRLRHFVATHASEP (SEQ ID NO:
91)

20 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCCTCC
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCAATTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACCTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGATATATATTTCTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCC
AAAATGCTGCTGCTTCTTGGTTCAATTCCACTACCATCCAGTTTGATGCTGTCTGCTGTACA
GATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT
25 GACCGGTGLIVHISAGLDSLLISFSYLLILKTVLGLTREAAQKAFGTCVSHVCAVFIFYVPFGLSM
VHRFSKRDSPLPVILANIYLLVPPVLNPVYGVKTKAIRQLRLRHFVATHASEP (SEQ ID NO:
92)

35

AOLFR49 sequences:

MLTFHNVCSVPSSFGLTGIPGLES�HVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAAILDLVLSSTIPKLLGIFWFGACDGLDACLQMFIAHLSGMESTVLLAMAFDRYVAICH
NPLRHSMLVTVTVVGRGLVSLRGVLYIGPLMIRLRLPLYKTHVISHSYCEHMAVVALTC
40 GDSRVNMVYGLSIGFLVLILDSVAIAASYVMIFRAVMLATPEARKLTGTCASHLCAILIFYVP
IAVSSLHFRFGQCVPPPVTLLANFYLLIPILNPVYAVRTKQJRESLLQPIRIEMKIR (SEQ ID
NO: 93)

45 ATGCTCACCTTTTCAATAGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCAGG
GCTGGAGTCCCTACAGTCTGGCTCTCCATCCCTTGTGCTCAATGATCACTGGTGGCTGTG
GTGGGGAATGTGACCATCTGGCTGTGGTAAAGATAGAACCGCAGCTGCACAGCCCATG
TACTTTTCTGTGACATGTTGGCTGCCATTGACCTGGTCTGTCTACTTCCATATACCCAA
ACTCTCGGGAATCTTCTGGTTCCGTGCTTGTGACATTGGCCTGGAGCGCTGCTGGGCCAA
ATGTTCCCTATTCCACTGCTTGGCACTGTTGAGTCAGGCATCTTCTTGGCATGGCTTTTGA
50 TGCTCATGTGGCCATCTGCAACCCACTACGTCATAGCATGGTCTCACTTATACAGTGGTG
GGTCTGTTGGGGCTTGTCTCTCTCCCGGGGTGTTCTACATTGGACCTCTGCCTCTGAT
GATCCGCTGCGGGCTGCCCTTTATAAAACCATGTTATCTCCCACTCACTGTGAGCAC
ATGCGTGTAGTTGCTCTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTCTGGTGTGATCTGGACTCAGTGGCTATTGCTGCATCTATGATGATTTT
55 CAGGCGCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCTGGGGACATGCGC
TTCTCACTCTGTGGCATCTGATCTTTATGTTCCCAATTGCTGTTCTTCCCTGATTCACCG

ATTTGGTCAGTGTGTGCTCTCCAGTCCACACTCTGCTGGCCAACTTCTATCTCCTCATTC
CTCCAATCTCTCAATCCCATTTGTCTATGCTGTTGCGACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

5 **AOLFR50 sequences:**

MNLDSSFFSLLKSLIMLNSSSWRLPQPSFFLVGIPGLEESQHWIALPLGLYLLALVGNVTILFII
WMDPSLHQSMYLFILSMLAADLVVASTAPKALAVLLVRAQEIGYTVCLIQMFHTAFSSMES
GVLVAMALDRYYAICHLPHHSTILHPGVIGHGMVVLVRGLLLIPFLILRLKLIQCQTIIGHAY
CEHMAVVKLACSETTVNRAYGLTVALLVVGDLVLAIGVSYAHILQAVLKVPGNEARLKAFST
CGSHVCVLIFYRPGMFSFLTHRFGRHVP HHVHVLLAILYRLVPPALNPLVYRVKTKIHQ
(SEQ ID NO: 95)

ATGAATTGGGATTCTTTTTTCTCTTCTCTCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGGAGGCTACCCAGCCTTCTTTTTCTCTGGTAGGAATTCCGGGTTTAGAGGAAAGC
CAGCACTGGATCGCACTGCCCTGGGCATCTTTACTCTCTGTCTAGTGGGCAATGTIA
15 CCAITCTCTCTCATCTGGATGGACCACTCTTGCAACCAATCTATGACCTCTTCTGTCTC
ATGCTAGCTGCCATCGACCTGGTGTGTGGCCTCTCTCACTGCAACCAAGCCCTTGCAGTGC
TCCTGGTTCGTGGCCAAAGAGATTGGTTACACTGTCTGCTGATCCAGATGTTCTTCAACCAT
GCATTCTCTCTCCATGGAGTCAGGGGTACTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
20 TTTGTCAACCCCTTGCACCATTCACAAATCTGCATCCAGGGGTGCATAGGGGCACATCGGAAT
GGTGGTGTCTGGTGGGGGATTACTACTCTCATCCCCCTTCTCATTTCTGTGGCAAAACTT
ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAC
TTGGCTGCTCAGAAACACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTGTCTGTGGT
TGGGCTGGATGTCTTGGCCATTGGTGTTCCTATGCCACATTTCCAGGCAAGTGTCTGAAG
25 GTACCGAGAAATGAGGCCCGCACTTAAGGCCTTTAGCACTGTGGCTCTCATGTTGTCTICA
TCTTGGTCTTCTATATCCCGGAATGTTCTCTTCTCTCACTACCGCTTTGGTTCATCATGTA
CCCCATCAGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGTCACTCAATCC
TCTTGTCTATAGGTGAAGACCCAGAAGATCCACCACTGA (SEQ ID NO: 96)

30 **AOLFR51 sequences:**

MCQQLRDGILLIHLINRKKVSLVMLGPAYNHTMETPASFLLVGIPQLQSSHLWLAISLSAM
YIALLGNITIVTAIWMDSRHEPMYCFCLVLAADVIVMASSVVPKMVSIFCSGDSISSFASCTFQ
MFFVHLATAVETGLLLTMAFDRIYAICKPLHYKRLTPQVMLGMSMAITIRAIATPLWSMVS
HLPFGCSNVVVHVSCEHIALARLACADVPVSSLYSLGSSLMVGSDBAFAIASYILKAVFGLSS
35 KTAQLKALSTCGSHVGMALYYLPGMASIYAALWGDVVPVPLHTQVLLADLYVIIPATLNPIHY
GMRTKQLRERIWSYLMHVLFDSHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAACCTTACGGGATTGCACTTCTCTCATACATCATTGTGTCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTAAACCAACAATGGAAACCCCTGCCTC
40 CTCTCTCTTGTGGGTATCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGA
GTGGCATGTACATATAGCCCTGTTAGGAAACACCATCATCGTCACTGCAATCTGCATGGA
TTCACTCGGCATGAGCCATGTATTGCTTCTGTGTGTTCTGGCTGCTGTGGACATTTGTA
TGGCCTCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGTCTGTTTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAAGCGGGG
45 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCATACATAAAGA
GAATCTCACGCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATACTCACTGAGTGTGGATGGTGAGTCACTACCTTTCTGTGGCTCCAAATGTGGT
GTCCACTCTACTGTGAGCACATAGCTTTGGCCAGGTATGAGTGTGCTGACCCGTGGCCCA
CGAGTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCTTCATGTCT
50 GCCTCTATATCTTAATTTCAAGGCAGTATTGGTCTCTCCAAGAGACTGCTCAGTGTGAA
AGCATTAAGACATGTGGCTCCCATGTGGGGGTATGGCTTTGTACATATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTGGGGCAGGATGATGTCCTTGACACACCAAGCTCTGCG
TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
55 CAAACAACTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAACT
CTGGGTTCATGA (SEQ ID NO: 98)

09865055-062201

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAIISLSAMYITALLGNTLJVTAIWMDSTRHEPMY
CFLCVLAADVIVMASSVVPKMMVSIFCSGDSISFSACFTQMFFVHLATAVETGLLLTMAFDRYV
AICKPLHYKRLITPQVMLGMSMAVTRAVFTMTPLSWMMNHLPCFGSNVVVHSYCKHIALAR
LACADPVPPSSLYSLIGSSLMVGSDEVAFIAASYILIRAVFDLSSKTAQLKLSTCGSHVGMALY
YLPGMASIIAAWLGQDIVPLHTQVLLADLYVIIPATLNPYIGMRKQLLEGITWSYLMHFLFDH
SNLGS (SEQ ID NO: 99)

- 10 ATGCTGGGTCCAGCTTACAACACACAATGGAAACCCCTGCCTCCTCTCTTGTGGGTA
TCCCAAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGAGTGCCATGACATCAC
AGCCCTGTATTAGGAAACACCCCTATCGTGACTGCAATCTGGATGGATTCACTCGGCATGAG
CCCATGTATTGCTTTCTGTGTGTCTGGCTGCTGTGGACATTTGTTAGGCCCTCCTCCGTGGT
ACCCAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTTGTTT
ACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGAOCCATGG
15 CTTTGTACCCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAAATTTCTACGCCTCA
AGTGATGCTGGGAATGAGTATGGCCGTCAACATCAGAGCTGTCACATTCATGACTCCACTG
AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA
GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGCTCTCTACAGTCTG
ATTGGTCTCTCTTATGTTGGGCTCTGATGTGGCCTTCATTGCTGCCTCTATATCTTAAT
20 TCTCAGGGCAGTATTGTATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT
GGCTCCCATGTGGGGGTTATGGCTTTGACTATCTACCTGGGATGGCATCCCATCTATGCGG
CTTGTTGGGGCAGGATATAGTGCCCTTGACACCCCAAGTGTGCTAGCTGACCTGTACGT
GATCATCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTCGTGGAG
25 GGAATATGGAGTATCTGATGCACTTCTCTTTGACCACTCCAACCTGGGTTTCATGA (SEQ
ID NO: 100)

AOLFR54 sequences:

MSDSNLSNDNHLPTFTFLTGIPGLEAAHFWIAIPFCAMYLVALVGNAAALIVIAMDNALHAPMY
LFCLLSLTDLALSSTVTPKMLAILWLHAGEISFGGCAQMFCVHSIIALESSILLAMAFDRYVA
10 ICNPLRYTILNHAVIGRIGFVGLFRSAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGRIARACA
NITVNIVYGLTVALLAMGLDSILIAISYGFIHVAFHLPSHDAQHKALSTCGSHIGILVFYIPAFF
SFLTHRFHGHEVPKHVHIFLANLYVLVPPVLPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
NO: 101)

- 35 ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
CAGGGCTGGAGGCTGCCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTGTAGC
ATGTTGGTGGAAATGCTGCCCTCATCTGGTCATTGCCATGGCAAAATGTCTTCTATGCACCT
ATGTACCTTCTCCTCTGCCCTTCTCTCACTACAGACCTGGCTCTCAGTTCTACCACTGTGCC
40 AAGATGTGGCGCCATTTTGTGGCTCCATGCTGGTGAGATTCTCTTGGTGGATGGCTGGCC
CAGATGTTTGTGTCCATTCTATCTATGCTCTGGAGTCTCGATTCTACTTGGCATGCCCTTT
TGATAGGTATGGGCTATCTGTAACCCATTAAGGTATACAACCACTTCTCAACCATGTGCTC
ATAGGCAGAAATGGCTTTGTGGGCTATCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
CTTGCTGAGGGCGACTCCCTACTGTGGTACCCTGTGCATGACACACATACTGTGAGCAT
ATGGGCATCGCCCGACTGGCCTGTGCAACATCACTGTCAATATTGTCTATGGGCTAACTG
45 TGGCTCTGCTGGCATGGGACTGGATTCCTTCTCATTTGCCATTCTCATTTGCCCTTATCTCTC
CATGCAGTCTTTCACCTTCCATCTCATGATGCCAGCAGCAAGAGCTGTGATGACCTGTGGCT
CCACATTTGGCATCATCTGGTTTTCTACATCCCTGCTTCTCTCTCTCAACCCCAAGCCTG
TTTGGTCAACCAAGATCCCAAGCATGTGCACATCTTTCTGGCTAATCTCATGTGCTGTG
50 TGCTCTGTCACTCAATCTTCTATGAGGACTAGAACCAAGAGATTGCGGAGTCGACT
TCTAAACTGCTTCACTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYLHWTEKSNSTLFIILLGFSQNKNEIYLCVFLFCYIAIWMGNLLIMISITCQ
LHQPVMYFFNLNLSLDLCYSTVTPKLMVDLLAERKTSISYNNCMIQLFTTHFFGGIEFILFTGM
10 AYDRVYAIKPLHYTMSRQKCNTHIIVCTGGFHSASQFLFTIFVPCGPNEDHYFCDVYPLL
KLACNSNIHMIGLLVIANSGLIALVTFVVLSSYVFILYTIRAYSAERRSKALATCSSHVIVVVLFF

APALFYIYRPVTTFSDEKVFALFYTHIAPMFNPLYTLNRNTEMKNAMRKVWCCQILLKRNQLF
(SEQ ID NO: 103)

5 ATGTCATTTCAGGTGACTTATATGTTCTATCTACACTGGACCATTGAAAAAGCAATAATA
GCACCTTGTGTTATCTCTGGGGTTTTCCCAAAATAAGAACATTGAAGTCCTCTGCTTTGTA
TTATTTTGTGTTGATGCATCTGCTATTTGGATGGGAACTTACTCATATGATTTCTATCAC
GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCCTCAATTACCTCTCACTCTCCGACC
TTTGTCATACATCCACAGTGACCCCAAAATTAATGGTTGACTTACCTGGCAGAAAGAAAGAC
TCTTTCCTATAAAGTGTATGATACAACTCTTACCACCCATTTTTTGGAGGCATAGAGA
10 CTTCAITCTICACAGGATGGCCTATGACCGCTATGTGGCCATTGCAAGCCCTGCACTA
CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA
TTTATACATTCTGCCAGTCAGTTCTCTCACCATCTTTGTACCAATTTGTGGCCCAAAATGA
GATAGATCACTACTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
15 TGATAGGTCTCTTAGTCATTGTCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG
TTGTTGTCTTATGTTTTATATTGTATACCATCAGAGCATACTGCGAGAGAGACGACGA
AAGCTCTTGCCACTGTAGTTCATGTGAATTGTTGGTGCTCTGTTTTTGCTCCTGCACTTG
TTCATTACATTAGACCGGTCAACAACATCTCAGAAGATAAAGTGTTCGCCCTTTTATATAC
CATCATTTGCTCCCATGTTCAACCTCTCTCATACAGCTGAGAAACACAGAGATGAAGAAC
20 GCGCATGAGGAAAGTGTGTTGTGTCAAATCTCTGAAAAGAAATCAACTTTTCTGA (SEQ
ID NO: 104)

AOLFR58 sequences:

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNSFVTEF
VLLGLSNPNVQEIFVVFVLYIATVGGNMLIVVLTSSPALLVSPMYFLGLSFLDACFSSVI
25 PTKMIVDSLYVYTKTISFEGCMMLQFAEHFFAGVEVIVLTAMAYDRYVAILKPLHYSSIMNRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHEMCDLYPLELACTDTHIFGLMVVNSG
FICINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVILFFVPCIFVYTRPSPAFSLDKMA
AIFYIILNPLLNPLYITFRNKEVKQAMRRIWNLMLMVVSEKENIKL (SEQ ID NO: 105)

30 ATGTTCTCATGACAACAGAAGCACTCAATAATTTTGCACTGGATGTACCAACTTGTATA
TGACTATTGATACCCAAAATTGATCTGAAGCAAAATTTTCCTTTGTCTCAATTGCGAGACTATA
CATGATCCCTGTTGGAGCTTTTATCTTTTTCCTTGGGAAACATGCAAAACCAAGCTTTGTA
ACTGAGTTTGTCTCCTGGGACTTTCACAGAATCCAAATGTTACAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTCGAACCTGTGGGGGCAACATGCTAATTGTAGTAACCATCTCT
35 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTCTTCTGGGCTTCTGCTCCTCTGGA
TGCGTGCTTCTCATCTGTCATCACCCCAAGATGATTGTAGACTCCCTCATGTGACAAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTHTCTTGTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
40 GGCCTTTGCAATCCATGATACAAAATCTTTTACTTTCCAGATTCCTCTTTGTGGCCCAAG
TGTCATCAATCACTTATGTGTACTGTACCGGTACTGGAGCTTGCTGCACCTGATACTG
ACATCTTTGGGCTCATGGTGGTGCATCAACAGTGGGTTTATCTGCATCAAACTCTCTCTG
TTGCTTGTCTCCTATGCTGTCTCTTGTCTCTCTGAGAACACACAGTCTGAAGGGCGCTG
GAAGACTCTCTCCACTGTGGATCTACATGCTGTTGTGATTTGTTCTTTGTGCCATGCA
45 TATTTGTATATACAGCACTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTTCAGGAATAAGGAAGTAAAC
AGGCATGAGGAGAATATGGAACAGACTGATGGTGTGTTCTGTAGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 106)

AOLFR59 sequences:

MGDWNNSDAVEPIFILRGFPGLEYVHWSLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYYFI
SILAVNDLGMSTLSTPLMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
PLPHYPTILNSVIGIKGLACLRLSGVVLPTPLLRHYHYCHGNALSHAFCLHQDVLRLSCDTA
TRNSIYGLCVVIATLGVDSIFILSYVLILNTVLDIASREEQLKALNTCVSHICVFLFFVPVIGVS
55 MVHRFGKHLSPVHILMADIYLLPVLNPIVYSVRTKQIRLGILHKFVLRFRF (SEQ ID NO:
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTCTCTG
GACTGGAGTAGTTCATCTCTGGCTCTCCATCCTCTCTGTCTTGCAATATTTGGTAGCATTTT
ATGGGTAATGTTACCATCTGTCTGTCTGATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA
5 TTACTTTATTTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCTGTCTACACTTCCACCA
TGCTTGTCTGTGTTATGTTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGTCTATGCTCAGCT
GTCTTCTACACACATTTACATTTCTGGAAGTCTCCAGTGTTGCTGGCCATGGCCCTTTGACC
TTTGTGTTGCTATCTGCCATCCACTGCACTACGCCACCATCTCACCAACAGTGTAAATTTGGC
10 AAAATTTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTACTTCCCACACCTTTGTCTACT
GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCAGCCTTCTGTTTGCACACAGGAT
GTTCTAAGATTATCTCTGACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
TTGCCACACTAGGTTGGATTCAATCTTCACTCTTCTTATGTCTGATCTCTTAATACT
GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCCTCAACACATGTGTATCCCAT
TCTGTGTGGTGCTTATCTTCTTGTGCCAGTATTGGGGTGCTAATGGTCCATCGCTTTGGG
15 AAGCATCTGTCTCCCATAGTCCACATCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT
CCTTAACCTATTGTCTATAGTGTGAGAACAAAGCAGATTGCTCTAGGAATTCTCCACAA
TTTGCTCAAGGAGGAGGTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

20 MFLPNDTQFHPSFELLGIPLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMPFYFLA
MLATTDVGLSTATIPKMLGIFWINLRGIIEACLQMFHFNFTLMESAVLVAMAYDSYVAICN
PLQYSAILNKVSVVIGLVFVRALIFVIPSILLILRPFCCGNHVPHTYCEHMGHLHLSKASIKINI
IYGLCAICNLVFDITVIALSYVHILCAVFRLPITHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
FGRNVPRVHIIILANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF
25 (SEQ ID NO: 109)

ATGTCTCTTCCCAATGACACCCAGTTTACCCCTCCTCCTCTCTGTGTGCTGGGGATCCCAGG
ACTAGAAACAATTCACATCTGGATCGGCTTCCCTTCTGTGCTGTGATACATGTATGCACTC
30 ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCTACACCAAGCCCTATGT
TCTACTTCTCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCCAA
GATGCTTGGAAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCAACCCAG
ATGTTTTTTATCCCAACTTCACACTTATGGAGTCAGCAGTCTTGTGGCAATGGCTTATG
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCTCTACCAACAAGGTTGT
TTCTGTGATTTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTGTGCTATCCCTCTATACTTC
35 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAAATCCCCACACCTACTGTGAGCACAT
GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATATTATATGGTTTATGTGCCA
TTTGAATCTCGGTGTTTGACATCACAGTCATTGCCCTCTCTTATGTGCAATATCTTTGTGCT
GTTTTCCTCTTCTCATCTATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTTCACTATGT
40 GTGTGGTCCCTTGGCTTCTATACACAGCCCTCTTTCCCTTATGACTCAATGTCTTTGGCC
GAAATGTGCCCGCTATATCCATATCTCTAGCCAAATCTCTATGTTGTGGTGCCACCAAT
GCTCAATCCTGTATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT
ATTATTGAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
(SEQ ID NO: 110)

AOLFR61 sequences:

45 MSIINTSYVEITTFVLVGMGPLEYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHGPMPYFVLSML
AMSDLGLSLSSLPVLISFLNAPETSSACFAQEFFIHGFSVLESSVLLMSFDRFLAIHNPRLYT
SLTTLVRVAQVIGVSEFKSMMLVLPFPFTLRSLRYCKKNQLSHSYLILHODVMKLACSDNRDVIY
GFFGALCLMVDIFILIAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFYLPIINLAVNHRFAG
50 HVSPLINVLMANVLLLVPMLMKPIVYCVKTKQIRVRVVAKLQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATGTCTATT
35 CTAGGAAATGGCAACATCTTCTTTATCATCAAGACAGAGCCCTCTGTGATGGGCCCAATGT
ACTATTTTTCTTCCATGTGGCTATGTGAGACTTGGGTTGTCTTATCATCTCTGCCCACT
GTGTTAAGCATCTTCTGTTCATATGCCCTGAAACCTTCTTCTAGTGCTCTGCTTTGCCACGGA

ATTTCTTCATTGATGGATTCTCAGTACTGGAGTCTCAGTCTCTGATCATGTGATTGATA
GATTTCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGATTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTTACATT
TAAGAAGCTTGAGATTGCAAGAAAAACCAATTATCCCATTTCTACTGTCTCCACCAGGA
5 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTGTGGAGCA
CTCTGCCATTATGGTAGACTTTATTTCTCATTGCTGTGTCTTACACCTGATCCTCAAGACTGT
ACCGGGAATTGCAATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACCTTGTGTTTCAACATC
TGTGCAGTGATCATCTTCTACCTGCCATCATCAACCTGGCCGTGTGCCACCGCTTTGCCGG
GCATGTCTCTCCCTCATTAATGTCTCATGGCAAAATGTTCTCCTACTGTACCTCCGCTGA
10 TGAAACCAATTGTTTATTGTGTAAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGTCATGGAAGATTAA (SEQ ID NO: 112)

AOLFR62 sequences:

MFYHNKSIFHPVTFFLIGIPLEDHFMWISGFPCSVYLVALLGNATILLVIKVEQTLREPMFYFL
AILSTIDLALSATSVPRMLGIFWEDAHEINYGACVAQMFLIHAFMGAEVLLAMAFDRYVAIC
15 APLHYATILLTSLVLVGISMCIIVRPLLTPMVLYLYRLPFCQAHIIHASYEHMGLAKLSCGNIRI
NIGYGLFVVSFFVLNLVLIGISYVYLRAVFRPLPSHDAQLKALSTCGAHVGVICVFYIPVSFSLT
HRFGHQIPGYIHILVANLYLIIPPSLNPHIYGVRKQIRERVLYVFTKK (SEQ ID NO: 113)

20 ATGTTTATCAACAAGAGCATATTTACCCAGTCACATTTTTCTCATTTGGAATCCCGAG
TCTGGAAGACTTCCACATGTGGATCTCGGGCCCTTTCTGCTCTGTTTACCTTTGCGCTTTGC
TGGGCAATGCCACCATTTCTGCTAGTCAATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT
CTACTCTCTGGCCATTCTTTCCACTATTGATTTGGCCCTTTCTGCAACCTCTGTGCTCGCA
TGCTGGGTATCTCTGGTTTGATGCTCACGAGATTAACTATGGAGCTTGTGTGGCCAGAT
25 TTTCTGATCATGCCCTTCACTGGCATGGAGGCTGAGGCTTACTGGCTATGGCTTTTGTAGC
CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGTGT
GGCATATGATCATGTGCAATTGTAATTCGTCCCGTTTACTTACACTCCCATGGTCTATCTTA
TCTACCGCTACCTCTTTGTGACGGCTACATAATAGCCCATCTTCACTGTGAGCACATGGG
CATTGCAAAATTTGCTCTGTGGAACATTCGTATCAATGGTATCTATGGGCTTTTGTGATGTT
30 TTTCTTTGTTCTGAACCTGGTGCTCATTTGGCATCTCGTATGTTTACATCTCCGTGCTGT
TTCCGCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCAGCTGTGGCGCTCATGTG
GAGTCACTGTGTTTCTATATCCCTTCACTGCTCTCTTCTTCTTCACTCATCGATTGGACAC
CAAAATACAGGTTTACATTCATCTCTGTTGCCAATCTCTATTGATTATCCCACCTCTCT
CAACCCCATCTTATGTTGGGTGAGGACCAACAGATTCGAGAGCGAGTGCTCTATGTTTTT
35 ACTAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSINTSYVEITFFLVGMPGLEAHIWISIPICSMYLIALLGNGTILFIKTEPSLHEPMYYFLSML
AMSDLGLSSSLPTVLSIFLNAPEISSNACFAQEFFIHGFSVLESSVLLIMSDFRFLAIHNPLRYTS
40 ILTTRVVAQIGIVFSFKSMILLVLPFFTLRNLRYCKKNQLSHSYCLHQDVMKLCASDNRIDVY
GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFLIPIINLAVVHRFAR
HVSPLINVLMAVNLVLPPLTNPIVYCVKTKQIRVRVVAKLQRKJ (SEQ ID NO: 115)

45 ATGTCCATTATCAACACATCATATGTTGAAATACCACCTTCTTCTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATGCTATT
CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGATAGGCCCATGT
ACTATTTTCTTCCATGTGGCTATGTCAGACTTGGGTTGTCTTTATCATCTCTGCCCAT
TGTTTAAGCATCTTCTGTTCAATGCTCCTGAAATTTCATCCAATGCTGCTTTTGCCAGGA
ATTCTTCATCATGGATTCTCAGTACTGGAGTCTCAGTCTCTCCTGATCATGTCAATTGATA
50 GATTCTAGCCATCCACAACCTCTGAGATACACCTCAACTCTGACAACCTGTCAGAGATTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTTCACTT
TAAGAAATTTAGATATTGCAAGAAAAACCAATTATCCCATCTCTACTGTCTGCCACAGGA
TGTCAAGTAAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTGTGGAGCA
CTCTGCCATTGTTAGACTTTATTCTCATGTGTGTCTTACACCTGATCTCAAGACTGT
55 ACTGGGAATTGATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTGTGTTTACACATC
TGTGCAGTGATCATCTTCTACCTGCCATCATCAACCTGGCCGTGTGCCACCGCTTTTGCCCG

GCATGTCTCTCCCCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
CGAACCCCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGTCAACGGAAGATTAA (SEQ ID NO: 116)

5 **AOLFR64 sequences:**

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTVLGNLTILHVICTDALTLHGPMYYFLG
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
HDSVTVLTPACIVKMGLSVLSALLJLPLFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIVN
HIYGLFVVACTVGVDSLLIFLSYALILRTLVSIAHQERLRLALNTCVSHICAVLLFYFPMIGLSLV
10 HRFGEHLPRV VHLFMSYVYLLVPPLMNPFIYSIKTKQIRQRJIKKFQIKSLRCFWKD (SEQ ID
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAGAGCCACTTTCTTCTGACGGGCTTCCAAG
GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTCTGCTTCATCTACCTGACAGTTATC
15 TTGGGGAACCTCACCATCTCTCCACGTCATTGTACTGATGCCACTCTCCATGGACCATGT
ACTATTTCTTGGGCATCTAGCTGTACAGACTAGGCCCTTTGCCCTTTCCACACTGCCACT
GTCTGTGGCATTTTCTGGTTGTATACAGAGAGATTGGCATCCCTGCTGTTCTCACTCAGC
TGTCTTCTACCCACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCATTGAC
CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCTGACACTGCATGTATTG
20 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCTTGGCAATTCCTC
CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATGTCTTACCTGGGA
GATCATGAAGCTGGCCGTCTCTAGCATCATTTGTCATACATCTATGGGCTCTTTGTGTG
CGCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCCTTCGCAC
CGTGTCTCAGCATTGCTCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
25 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTGTGCTCTTGTGCATCGCTTTGG
TGAACATCTGCCCGCGTGTGTACACCTCTTCTATGTCCTATGTGTATCTGCTGGTACCAACCC
TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAGAA
GTTTCAGTTTATAAAGTCACTTAGGTGTTTGGGAAGGATTA (SEQ ID NO: 118)

30 **AOLFR65 sequences:**

MAGRMSTSNHTQFHPSSFFLLGIPGLEDVHIWIGVPPFFVYVALLGNTALLFVIQTEQSLHEPM
YYFLAMLDSIDLGLSTATIPKMLGIFWNTKEISFGCLSHMFFHHFFTAMESIVLVAMAFDRYI
AICKPLRYTMILTSKIIISLAGIAVLRSLYMVVPLVFLLLRLPFCGHRIIPHTYCEHMGJARLACAS
IKVNIRFGLGNISLLLLDVILIISYVRILYAVFCLPSWEARLKALNTCGSHGVILAFFTPAFFSFL
35 THRFHGNIPQYIHIILANLYVVVPPALNPVYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCATCCTTCTTCTTCTTCTTCTGCT
GGGTATCCACGGGCTAGAAGATGTGCACATTTGGATGGAGTCCCTTTTCTTTCTTGTGTAT
CTTGTGTGCACTCCTGGGAAACACTGCTCTCTGTGTGTGTATCCAGACTGAGCAGAGTCTCC
40 ATGAGCCTATGTACTACTTCTCGCCATGTTGGATTCCATTGACCTGGGCTTGCTACAGC
CACCATCCCAAAATGTTGGGCATCTCTGTGTTCAATACCAAGAAATATCTTTTGGAGGC
TGCTTTCTCACATGTTCTTCTATCCATTCTTCTACTGCTATGGAAGACATTTGTGTGTGTGGC
CATGGCCTTTGACCGCTACATTGCCATTGCAAACTTTCGGTACACCATGATCTTCACCA
GCAAATACATCAGCCTCATTTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTTGTTC
45 ACTGGTGTCTTCTCTCTGAGGCTGCCCTTCTGTGGGCATCGCTATCATCCCTCATACTTATT
GTGAGCACATGGGCATTGCCGCTGTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG
CCTTGGCAACATATCTCTCTGTGTACTGGATGTTATCTCTTATTTCTCTCTATGTACAGGA
TCTGTATGCTGTCTCTGCTGCCCTCGCCCTCGGGAAAGCTCGACTCAAAGCTCTCAACACTGT
GGTCTCATATTTGGTGTATCTTAGCCTTTTTACACCAGCATTTTTCATCTTTTGACACA
50 TCGTITTTGGCCATAATATCCACAGTATATACATATTATATTAGCAACCTGTATGTGGTTG
TCCACCAAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTTCGAGAGAGAG
TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

55 MSFLNGTSLTPASFILGIPGLEDVHLWISFPLCTMYSIATIGNFLMYLIYDEALHRPMYVFL
ALLSFTDVLMTCTSLPTNLFILWFNLKEIDFKACLAQMFFVHITPGMESGVLMMLALDHCVAI

093605-06204

CFPLRYATILTNSVIKAGFLTLRGLVMLVIPSTFLTKRLPYCKGNVPHITYCDHMSVAKISCGN
VRVNAIYGLIVALLIGGGFDILCTISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLYTVPAFF
TFTTHFGGHTIPLHIHIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGKDNSHNF (SEQ
ID NO: 121)

5

ATGTCATTCTAAATGGCACCAGCCTAACTCCAGCTTCATTATCTCTAAATGGCATCCCTG
GTTTGGGAAGATGTGCATTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT
ACAGGGAACCTTCGGCCCTATGTACCTCATCTACTGTGATGAGGCCCTACACAGACCATGTGT
ATGCTCTCCTTGGCCCTTCTTCTCTACAGATGTGCTCATGTGACACGACCCCTCCCAAC
ACTCTCTCATATTGTGGTTAATCTCAAGGAGATTGATTTTAAAGCCTGCTCGCCAGAT
GTTCTTTGTGCACACCTTCACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
CACTGTGTGGCCATCTGCTTCCCTTGTGGTTATGCCACCATCTCACTAATTTCAGTCACTTGC
TAAAGCTGGGTCTCTCACTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTTCTCTCA
CCAAGCGCCTTCCATACTGCAAGGGCAACGCTCATACCCACACCTACTGTGACCACATGTC
TGTGGCCAAAGATACTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC
CTGCTGATTGGGGGCTTTGATATCTGTGCAATTACAATCTCTACACTATGATTCTTCAAGC
AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCCTCAGCACCTGCACTGCCAC
TTCTGTGCCATAGTCTCACCTATGTTCAGCCTTCTTTACCTTCTTTACACACCATTTTGG
GGGACACACCATTTCTCTACACATACATATTATATGGCTAACTCTCACTACTAATGCCTC
CCACAATGAACCTATTGTGTATGGGGTGAAGAACAGCAGGTACGAGAAGGTGTCATTA
GGTTCTTTCTTAAGGGAAAGGACAATTCTCATACCTTTTAA (SEQ ID NO: 122)

10

15

20

AOLFR67 sequences:

MSGDNSSSLTPGFFLIVGVPGLEATHIWISLPFCFMYIIHAVVGNCGLICISHEEALHRPMYFLA
LMSFTDVTLLCTTVMFVNMCLCFWFLKEIDFNACLAQMFVHMLTGMESGVLMMLMALDRYVAI
CYPLRYATILTNPVIKAGLATFLRNVMILHPTLLTKRLPYCRGNFPHITYCDHMSVAKVSCGN
FKVNAIYGLMVALLIGVDFDICISVSYTMILQAVVMSLSSADARHKAFTSTSHMCSIVITYVAFF
TFTTHFRFVGHNPNIHIIVANLYLLPPTMNPVYGVKTKQIQEGVIRFLLDGKVSFTYDK
(SEQ ID NO: 123)

25

30

ATGTCCTGGGGACAACAGCTCCAGCCTGACCCAGGATCTTTATCTTGAATGGCGTTCCTG
GGCTGGAAGCCACACACATCTGGATCTCCCTGCCAATCTGCTTTATGTACATCATTTGCTGTC
GTGGGGAACTGTGGGCTCATCTGCCTCATCAGCAATGAGGAGGCCCTGACCCGGCCCATGT
ACTACTCTCTGGCCCTGCTCTCCTCACTGATGTCACTTGTGACACCACTGTGTAACCTAAT
ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACCGCTGCTGGCCCA
TGTTTGTGTCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCTTACCAACCTCTGTCATG
CCAAGGCTGGTCTTGCACCTTCTTGAGGAATGTGATGCTCATCATCCCACTCACTCTCTCTC
ACCAAGCGCTGCCCTATTTGCCGGGGGAACCTCATCCCCACACCTACTGTGACCAATGT
CTGTGGCCAAAGGTATCTGCTGGCAATTTCAAGGTCAATGCTATTATGGTGTGTTGCTG
TCTCTGATTGGTGTGTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGACAGG
CTGTTATGAGCCTGCTATCAGCAGATGCTCGTCAAAAGCCTTCAGCAGCTGCACATCTCA
CATGTGTTCCATTGTGATCACCCTATGTTGCTGCTTTTTCACTTTTTCACCTCATGTTTGT
AGGACACAATATCCCAAACCATACACATCATGCTGGCCAACTTTATCTGCTACTGCTC
CCTACCATGAACCCAAATTGTTATGGAGTCAAGACCAAGCAGATTACGGAAGGTGTAATTA
AATTTTACTTGGAGACAAGGTTAGTTTACCTATGACAAATGA (SEQ ID NO: 124)

35

40

45

AOLFR68 sequences:

MTTHRNDLTSTEASDFLLNCFVRSPSWQHWLSLPSLLFLLAVGANTLLMTIWLASLHQPL
YVLLSLLSLDLIVCLTVIPKVLITIFWDLRPISFPACFLQMYIMNCFLAMESCTFMVMAVDYRY
VAJCHPRLYPSIHTDFHVVKAAAMFILTRNVLMTLPIPLSAQLRYCGRNVNIENCANMVSRLSC
DDVTNHLRYFAGGWLLGSDLILIFLSYFILRAVLRKAEGAVAKALSTCGSHFMILFFSTIL
LVFVLTHVAKKKVSPDPVLLNLVHHVIPAALNPIHYGVRTQEIQKGMQRLLKGC (SEQ ID
NO: 125)

50

55

ATGACAACACACCGAAATGACACCCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
 TGTGCAGATCCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCTCAGCCTCCTTTTCTCTTGC
 GCGTAGGGGCCAACACACCCCTCTGATGACCATCTGGCTGGAGGCTCTCTGACCCAGC
 CCGTGTACTACTGCTCAGCCTCCTCTCCCTGCTGGACAATCGTGTCTGCGCTCACTGTCATC
 5 CCAAAGTCTGTCAGCACTCTTCTGGTTTGACCTCAGGCCATCAGTCTCCCTGCTTCTCTC
 CCAGATGTACATATGAATTGTTTCTAGCCATGGAGTCTTGACATCATGGTCAATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCACTGAGATATCCATCAATCATCACTGATCACTT
 TGTAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCATCCCC
 ATCCTTTCAGCACAACTCCGTTATTGTGGAAGAAATGTCAATTGAGAACTGCATCTGTGGCA
 10 ATATGCTGTTTCCAGACTCTCTGCGATGATGTCCACATCAATCACTTTACCAATTTGCT
 GGAGGCTGGACTCTCTAGGATCTGACCTCATCTTATCTCTCTCTACACCTTCACTTCT
 CGAGCTGTGCTGAGACTCAAGGCGAGAGGGTCCGCTGGCAAAGGCCCTCAAGCACATGTGG
 CTCACACTTATGCTCATCTCTTCTTTCAGCACCATCCTTCTGGTTTGTGCTCACACATGT
 15 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGTCTCAATGTTCTCCACCATGTCAAT
 CCTGCAGCCCTTAACCCATCATTTACGGGGTGAGAACCAAGAAATTAAGCAGGGAATG
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

MSYSIKSTVNIPLSHGVVSHFCHNMNCFMHJFKFVLDFNMKNVTEVTLFVLKGFDTNLELQ
 20 TIEFFLFLAIYFTLMGNLGLILVVRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFITKN
 KIVTFLGCVAQVFLCAGSFGTTECFLLAAMAYDRYVAIYNPLLYSVMSPRVYMLPNLASVAGI
 LHATHIVTAFSLFCGANEIRRVFCDIPPLLAISYSDHTHTNQLLLFYFVGSIELVTILVLSYGLIL
 LAILKMYSAEGRKKVFSFSCGAHLTGVSIIYGTILFMYVRPSSSYASDHDIMVSIFYTIVIPLLNPV
 IYSLRNKDVDSMKMFMGKNQVINKVYFHTKK (SEQ ID NO: 127)

ATGTCGTACAGTATATACAAGGACAGTTAACTCCCTTGAGTCATGGTGTGTGTTCAAT
 CTTTTTGTCAATAATGAACGTGAACCTTTATGCATATCTTCAAGTTTGTCTAGATTCTCAAC
 ATGAAGAATGTCACTGAAGTACCTTATTTGTACTGAAGGCTTACAGACAATCTTGAAC
 30 TGACAGACTATCTCTCTCTCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA
 GGACTGATTTTGTGCTTATAGGATTCAGGATTCAGCTCCACAACCCATGTACTATTTCTGA
 GTATGTTGTCTTCTGTGGATGCTGCTATTCCTCAGTTATTACCCCAAAATATGTTAGTAGAT
 TTTACGACAAAAGAATAAAGTCAATTCATTCCTTGGATGTGTAGCAGAGGTGTTCTGTGCTT
 GTAGTTTGGAAACACAGAATGCTTCTTCTGGTGAATGGCTTATGATCGCTATGTAGC
 35 CATCTACAACCTCTCTCTGATTTCAGTGAGCATGTACCCAGAGTCTACATGCCACTATC
 AATGCTTCTATGTGTGCTGGCAATTTACATGCTACTATACATACAGTGGCTACATTTAGCCT
 ATCTCTCTGTGGAGCCAAATGAATAAGGCGTGTCTTTGTGATATCCCTCCTCTCTCTGTCTA
 TTTCTTATCTGTACACTACACAAACAGCTTCACTCTTCACTTTGTGGGCTCATCGAG
 CTGGTCACTATCCTGATGTTTCTGATCTCCTATGGTTTGATTCTGTTGGCCATTCTGAAGAT
 40 GTATTCTGCTGAAGGGAGGAGAAAGTCTTCCACATGTGGAGCTCACTAACTGGAGT
 GTCAATTTATATGGGACAATCCTCTTCAATGATGTGAGACCAAGTTCAGCATGTGCTCG
 GACCATGACATGATAGTGTCAATATTTACACCATGTGATTCCCTTGTGAATCCCGCAT
 CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA
 GGTATCAATAAAGTATATTTTCACTAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPKNKTEVTFMILTGFDTDFELQVFLFLFFAI
 45 YLFTLIGNLGLVVLVIEDSWLHNPMMYYFLSVLSFLDACYSYVTPKMLVNLAKNKSISFIGCA
 TQMLFLVTFGTTECFLLAAMAYDHYVAIYNPLLYSVMSPRVYPLITASVYAGILHATHIVA
 TFSLFCGSENIHVFCDMPPLLAISCSDDHTNQLLLFYFVGSIELVTILVLSISILKMHSA
 50 KGRQKAFSTCGSHLTGVTIYHGTILVSYMRPSSSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK
 KAVKMKMLKVYK (SEQ ID NO: 129)

ATGGACTCCACTTTTCAAGGCTATAACCTTTATAACCTGCAAGTAAAACTGAAATGGACA
 55 AGTTGTCACTCAGGTTTGGATATATACAGGAATCCACTGAAGAACAGACTGAAGTCCACA
 TGTTTATATTGACAGGCTTCACAGATGATTTGAGCTGCAAGTCTTCTATTTTACTATTTT
 TTGCAATCTATCTTTTACCTTGATAGGCAATTTAGGGCTGGTGTGTGTGGTCATTGAGG

098605-05201
 10220-55886

- ATTCCTGGCTCCACAACCCCATGTATTATTTCTTAGTGTTTATCATTCTTGGATGCTTGC
TATTTCTACAGTTGTACCTCCAAAATGTTGGTCAAATTTCTGGCAAAAAATAAATCCATT
CATTTATCGGATGTGCAACACAGATGCTTCTTTTGGTACTTTTGGAACTACAGAAATGTTTT
CCTTTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCTCTCTGTATTACGT
5 GAGCATGTACCCAGAGTCTATGTGCCACTCATCTGCTTCTACGTTGTGGCACTTTAC
ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCTTCTGTGGATCCAATGAAATAG
GCAATGCTTTTGTGATATGCGCTCCTCTCTGTGCTATTTCTGTCTGACACTACACAAAC
AGCTTCTACTCTTCTACTTTGTGGGTCTATTGAGATAGTCACTATCTGTATTGTCTCTATT
TCTCTGTGATTTCACTTGTGTGCCATTTCTGAAGATGCATTCTGTAAAGGGAAGGCAAAAGG
10 CCTTCTCTACATGTGGCTTCACTCACTAAGTGGAGTGACAAATTTATCATGGAACAAATCTCGTC
AGTTATATGAGACCAAGTTCACGCTATGCTTCAGACCATGACATCATAGTGTCAATATTT
ACACAATGTGTATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
AAAGGCAGTGAAGAAAATGTGAAATGTGTTTACAAATGA (SEQ ID NO: 130)
- 15 **AOLFR71 sequences:**
MGRNNNTNVPDFLTGLSDSEEVQMALFILLYLITMLGNVGMILIRLDLQLHTPMYFFLTH
LSFDLSYSTVITPKLANLLTSNYISFMGCFQAMFFVFLGAAEFCFLSSMAIDRYVAICSPRY
PVMSKRLCCALVTGPYVISFINSFVNVMWSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
MIHILAGSTLMVSLTISASYSVLSLSTILKINSTSGKQKALSTCASHLLGVTFYGTMTFYLKPRK
20 SYSLGRDQVASVFTYVIPMLNPLIYSLRKNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

- ATGGGTAGAGAAATAACACAAATGTGCTGACTTCATCCTTACGGGACTGTCAGATTCTG
AAGAGTCCAGATGGCCCTCTTATACTATTTCTCTGATATACCTAATACTATGCTGGGC
AATGTGGGATGATATGATAATCCGCTGGACCTCCAGCTTCACACTCCCATGTATTTT
25 TCCCTACTCACTGTGCTATTTATTGACCTCAGTTACTCAACTGTGTCATCACACTAAACCTTA
GGCAACTTACTGACTTCCAACATATATTCTCTCATGGGCTGCTTTGCCCAGATGTTCTTTT
TGTCTTCTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTAG
CTCTGCAAGCTCTCTACGTTACCCAGTTATTTATGCTGAAAAGGCTGTGTTGGCGCTCTGTG
30 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTGCAATGTGGTTTGGATGAGCAGAC
TGCAATTTCTGCGACATCAAAATGTAGTTCTGTCACATTTTCTGCGACACGCTCCAATTTTAGCT
CTGTCTGCAATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCACCCC
TGATGGGTGCCCTTATCACAATATCTGCACTCCTATGTGTCCATCTCTCTACCACTCCTGAAA
ATTAATTCACCTCAGGAAAGCAGAAAGCTTTGTCTACTTTGTGCTCTCATCTCTGGGAG
35 TCACCACTTTTATGGAACTATGATTTTTTACTTAATTAACCAAGAAAGCTTATTTCTTTG
GGAAGGGATCAAGTGGCTCTGTTTTTATACTATTGTGATTCCTATGCTGAATCCACTCAT
TTATAGTCTTAGAAACAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAAGACA
GGACTCCAGGTAA (SEQ ID NO: 132)

- AOLFR72 sequences:**
MAPENFRVTEFILTGVSSPELQIPLFLVFLVLYGLTMAGNLGHITLSVDSRLQTPMYFFLQHL
ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
YMVVSRRLCLLVSLTYLYGFTAIJVVSSYVFSVSYCSSNHNHFYCDNVPLLLALSCSDTYLPE
TSVNSAATNVVGLIILVSVFNIVLSILKICSSSEGRKKAFTSCASHMMAVTFYFGLLFMYVQP
RNNHSLDTDDKMASVFYTLVIPMLNPLIYSLRKNKDVKTALQRMTNLCYSFKTM (SEQ ID NO:
40 133)

- ATGGCTCCTGAAATTTTACCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
CAGAGCTCCAGATTTCCCTCTCTCTGGTCTTTCTGGTGTCTTATGGGCTGACCATGGCAGG
GAACCTGGGCATCATCCCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
50 TCTGCAACATCTGGCTCTCATTAATCTTGGTAACCTACTGTCACTTGGCCCTAAAAATGCTG
ATTAATCTTTTAGTAAAGAAAGAACTACCTCATTTCTATGAATGTGCCACCACTGGGAG
GGTTCTGTGCTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCTGTGACCCGAT
GTGGCTATTGTAACCTCTGCTGTACATGGTGGTGGTGTCTCGGGGGCTCTGCTCTCTGCT
GGTCTCCCTCACATCACTATGGCTTTTCTACAGCATTTGTGGTTTCACTCTTATGTAATCT
55 CTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTACTGTGATAATTGTCCTGTGA
GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA

- ATGTGGTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGCTATTTTAA
 AAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATTGATGG
 CAGTCACAATTTTATGGGACATTGCTATTATGATGTGCAGCCCCGAAGTAACCACTTC
 ATTGATCTGATGATGAAGATGGGCTTCTGTGTTTTACACGTGGTAAATTCCTATGCTGAAT
 5 CCGTTGATCTACAGCGTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
 AATCTGTGCTATTCTTTAAACAATGTAA (SEQ ID NO: 134)

AOLFR73 sequences:

- MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFLGLIILYLVTVIGNLGMVILTYLDSKLHP
 10 MYFFLRHLSTIDLGYSTVIAPKMLVNFVHKNTISYNWYATQLAFFEIFYSELFSAMAYDRYV
 AICKPLLYVIIMAEKVLVWLVIVPYLYSTFVSLFTIKLFLKFSFGSNIISFYDCDPLMSILCSDT
 NELELILIFSGCNLLFSLIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGLLLFIYL
 QPKSSHTLAIDKMASVFYTLILPMLNPLIYSLRNKEVDALKRRTLNRFKIPI (SEQ ID NO: 135)
- 15 ATGAATCATGTGGTAAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTTCTA
 TGGGGATTACAGACAACCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCTCATCATATA
 TCTGGTCTACAGTATGAGCAATCTGGGCATGGTATCTTGACCTACTTGGACTCCAGCTGA
 CACACCCCATGCTACTTTTCTTAGACATTTGTCAATCACTGATCTTGGTACTTCCACTGT
 CATTGCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG
 20 TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTTCTATCAGC
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGACGTGATCATATGGCA
 GAGAAAGTACTTTGGGTGCTGGTAATTGTCCTATCTCTATAGCACGTTTGTGTCACTATT
 TCTCACAATTAAGTTATTTAAACTGTCCTCTGTGGCTCAAAACATAATCAGCTATTTTACT
 GTGACTGTATCCCTCTGATGTCCATCTCTGTCTGACACAAATGAATTAGAATTAATAAT
 25 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCCCTCTCAATTGTCTCATATCCTACATGTT
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAGGGAGGTACAAAGCCTTCTCCACC
 TTAGAGCTCTCATGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACTGTGA
 ACCCAAGCTCAGTCATCTACTTGGCTATTGATAAAATGGCCTCAGTGTTTATACCTGTGTG
 ATTCTATGTGTAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAGATGCTCTAA
 30 AGAGAAGCTTAACCAATCGATTCAAAATCCCATTTAA (SEQ ID NO: 136)

AOLFR74 sequences:

- MEQHNLTVNFIILTGITDIAELQAPLFAFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
 35 LAEMDLGYSTVVGPKMLVNFVVDKNIISYFCATQLAFFLVFGSEILSAMSVDLYVAICNPL
 LYTIVMSRRVQVLVAIPPLYCTFISLLVTIKIFLTSFGYNVISHFYCDSPPLPLLCNSNTHIELI
 ILIFAIDLISSLLVLLSYLLJLVAILRMNSAGRQKAFSTCGAHLTVVIVFYGLLFMYVQPKSSH
 SFDDTKVASIFYTLVPMPLNPLIYSLRNKDVKYALRRVTWNLCNIFV (SEQ ID NO: 137)
- 40 ATGGAACAACACAATCTAACACCGTGAATGAATTCATTCTTACGGGAATCACAGATATC
 GCTGAGCTGCAGGCACCATTTATGTCATTGTCTCATGATCTATGATCTCAGTGATGG
 GCAATTTGGGCATGATTGTCTCACCAGTTGGACTCCAGGTGCAAAACCCATTATGACTTT
 TTTCTCAGACATCTGGCTTTCATGGATCTTGGTATTCAACAACCTGTGGGACCCAAAATG
 TTAGTAAATTTTGTGTGGATAAGAAATATAATTTCTATATTTTTGTGGCAACAGCATAGC
 45 TTTCTTTCTGTGTTTCATTGGTAGTGAACCTTTTATTTCTCAGCCATGTCCTACGAACCTCT
 ATGTGGCCATCTGTAACCCCTCTGCTATACACAGTAATCATGTGACGAAGGGTATGTCAGGT
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCAITCTCTTCTAGTACACATAAAGATT
 TTACTTTATCTCTGTGGCTACAACGTCAATAGTCATTTCTACTGTGACAGTCTCCCTTTT
 TTACTTTGCTTTGTGTCAAAATACACATGAAATGAAATGATAATTCGATTTTGCAGCAT
 TGAATTTGATTTCACTCTCTGATAGTTCTTTATCTTACCTGCTCATCTCTGTAGCCATTCT
 50 CAGGATGAATTTCTGCTGGCAGACAAAAGGCTTTTCTACCTGTGGAGGCCACCTGACAGTG
 GTCATAGTGTTCATGGGACTTTGCTTTTCATGTACGTGCAGGCCAAGTCCAGTCACTCTCT
 TGACACTGATAAAGTGGCTTCCATATTTACACCTGGTTATCCCATGTTTGAATCCCTTGA
 TCTATAGTTTACGAACAAAGATGTAAATATGCCCTACGAAGGACATGGAATAACTTATG
 TAATATTTTGTGTTAA (SEQ ID NO: 138)

AOLFR75 sequences:

- MEGKNQTNISEFLLGFSSWQQQVLLFALFLCLYLTGLFGNLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNQITQTITISYPGCLAQMYFCMMFANMDNLLTVMAYDRYVAI
 CHPLHYSTIMALRLCASLVAAPVWVAILNPLHLTMMMAHLHFCSDNVIIHFFCDINSLPLSCSD
 5 TSLNQLSVLATVGLFVVPVSVILVSYILVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
 GVMYMSPLSNHSTEKDSAAVSVFMVVPVLNPFYISLRNNEKGLTKKTLSRPGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)
- ATGGAAGGGAAAAATCAACCAATATCTCTGAATTTCTCTCTGGGCTTCTCAAGTTGGC
 10 AACAACACGAGCGTGTCTACTCTTTGCACTTTTCTGTCTCTATTTAACAGGGCTGTTTGGGA
 AACTTACTACTCTTGTCTGGCAATTGGCTCGGACTACTGCCCTCACACACCCATGTATTTCTT
 CCTTGCCAATCTGTCTTGGTAGACCTCTGCCCTCAGCCACAGTCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCCTGGCTCAGATGTATTT
 CTGTATGATGTTTGGCAATATGGACAATTTCTTCTCACAGTGATGGCATATGACCGTTAC
 15 GTGGCCATCTGTCAACCTTTACATTACTCCACCATATATGGCCCTCGCGCTCTGTGCCCTCT
 GTTAGCTGCACCTTGGGTCAATTGCCATTTTGAACCTCTCTTGCACACTCTTATGATGGCCC
 ATCTGCACCTTCTGCTCTGATAATGTTATCCACCATTTCTCTGTGATATACACTCTCTCCTC
 CCTCTGTCTGTTCGACACCAAGTCTTAATCAGTTGAGTGTTCTGGCTACGGTGGGGCTGA
 TCTTTGGGTACCTTCAGTGTGTATCCTGGTATCCTATATCTCATTGTTTCTGCTGTGATG
 20 AAAGTCCCTTCTGCCAAGGAAACCTCAAGGCTTTCTCTACCTGTGGTCTGACCTGGTGTG
 GGTCACTCTTTTCTATGGAGCAACACAGGGGTCTATATGAGCCCTTATCCAATCACTCT
 ACTGAAAAAGACTCAGCCGATCATGCTATTTATGGTTGTAGCACCTGTGTGAATCCAT
 TCATTTACAGTTTAAAGAAACAATGAAGTGAAGGGGACTTTAAAAAAGACCTTAAGCCGGC
 CGGGCGGGTGGCTACGCCGTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
 25 TGAGGTCAAGGAGATCGAGACCATCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

- MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLGNLMIILILLDSLHPTMYFFLSNL
 30 GIGYSSAVTPKVLTLGLLIEDKAISYSACAAQMFFCAVATVENYLLSSMAYDRYAACVNPLHY
 TTTMTTRVCALGICYGVIGFLNASIQIGDIFRLSCFMSNVIIHFFCDKPAVITLTCDEKHISELIL
 VLISFNVFALLVTLISYLFILITLKRHTGKYQKPLSTCGSHLIAIFLYTTVIUMYIRPSSSHSM
 DTDKIASVFYTMIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)
- ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCGAGAA
 35 CTACAGGTTCCTCTTTATCATGTTTACCTCATCTACCTCATCATCTGACTGGGAACCT
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTCTCA
 GTAACCTGTCTTGTGACGCAATTGGTTACTCTCAGCTGTCACTCCAAAGGTTTAACTGG
 GTTGCTCTATAGAAAGCAAGACCATCTCCTACAGTGCCTGTGCTCAGATGTTCTTTTGT
 GCAGTCTTTGCCACTGTGGAAAATTACTCTTGTCTCAATGGCCTATGACCGCTACGCGAG
 40 CAGTGTGTAAACCCCTACATTATACCACCAATGACAAACAGTGTGTGTGCTGTCTGGC
 TATAGGCTGTTATGTCAATGGTTTCTGAATGCTCTTATCCAAATGGAGATATCTTCGCC
 TCTCTTTCTGCATGTCCAATGTGATTCATCACTTTTCTGTGACAAACAGCAGCATTAATCT
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTGTCTTATATCAAGTTTAAATGT
 CTTTTTTGCATCTCTGTACCTTGATTCTCTATCTGTTCATATTGATCACCATTCTTAAGAG
 45 GCACACAGGTAAGGATACACAGAAGCCTTATCTACCTGTGGTCTCACCCTATTGCCATT
 TTCTATTTTATATAACTGTCACTCATCATGTACATACGACCAAGTTCAGTCACTCCATGGA
 CACAGACAAAATTGCACTCTGTGTCTACACTATGATCATCCCATGCTCAGCTCATGTGCT
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTCATGAAGGTTGTTGAGAAGGCAAAAT
 ATTCTCTAGATTCACTCTTTAA (SEQ ID NO: 142)

50

AOLFR77 sequences:

- MGDVNQSASDFILVGLFHSRGLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFFLS
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFLLTLMGVAEGVLLVMSYDRYVAVC
 QPLQYPVLMRRQVCLLMMGSSWVGVNLASIQTSITLHFYPYASRIVDHFCEVPALLKLSA
 55 DTCAYEMALSTSGVLMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHTVGLFYGA

AVFMVMPCAIYHSPQQDNVSLFYSLVTPTLNPLIYSLRNPVWMALVKVLSRAGLRQMC
(SEQ ID NO: 143)

5 ATGGGGGATGTGAATCAGTCGGTGGCTCAGACTTCATTCTGGTGGGCTCTTCAGTCACT
CAGGATCAGCCAGCAGCTCTCTCTCCCTGGTGCGTGCATGTTGTTCATAGGCCCTCTGGGC
AACACCGTCTTCTCTCTCTTGATCCGTGTGGACTCCCGGCTCCACACACCATGTACTTCCT
GCTCAGCCAGCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCAACATCCCCAAGATGGCA
TCAGACTTCTTGGCGGGGAGAAGGTGCCACCTCTATGGAGGTGGTGACGTCAAATATCTT
TCTCAGCTATGGGGTGTGGCTGAGGGCGTCTGTTGGTCTCATGTCTTATGACCGTTA
10 TGTTCGTGTGTGCCAGCCCTGCAGTATCCTGTACTATGAGACGCCAGGTATGCTGCTG
ATGATGGGCTCTCTGGGTGGTAGGTGTGCTCAACGCCCTCCATCCAGACCTCCATCACCC
TGCAITTTCCCTACTGTGCTCCCGTATTTGGATGACTTCTCTGTGAGGTGCCAGCCCTA
CTGAAGCTCTCCTGTGCAGATACCTGTGCTACGAGATGGCGCTGCCACCTCAGGGGTGC
TGATCCTAATGCTCCCTCTTTCCTCATCGCCACCTCCTACGGCCACGTGTTGACGGCTGTT
15 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTACCACTGCTCCTCGACATCA
CGGTATGGGGCTCTTTATGGTGCCGCCGTGTTTCATGTACATGGTGCTTGGCGCTACCA
CAGTCCACAGCAGGATAACCTGGTTCCTCTTCTATAGCCTTGTCACCCCTACACTAAC
CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTTGGTCAAAGTGCTTAGCA
GAGCTGGACTCAGGCAATGTGCTGA (SEQ ID NO: 144)

20

AOLFR78 sequences:

MSPDGNHSSDPTFVLAGLPNLNSARVELFSVLLVYLLNLGNVLIVGVVRADTRLQTPMYF
FLGNLSCEILLTSVIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH
PLRYPLLMMSGAVCFRVALACVWVGLVPVLGPTVAVALLPFCQOGAVVQHFFGDCSPLRLIAC
25 TNRKLEELDFVLASLVVSSLLITAVSYGLIVLAVLSPISASGRQKAFSTCTSHLIVVTLFVGSAL
FLYVRPSQSGSVDTNWA VTVITFTVPLLPFFIYALRNEQVKEALKDMFRKV VAGVLGNLLD
KCLSEKAVK (SEQ ID NO: 145)

30 ATGAGTCCTGATGGGAACCACAGTAGTGATCCAACAGAGTTCTGCTCGGCAAGGCTCCCA
AATCTCAACAGCGCAAGAGTGGAAATATTTCTGTGTTCTTCTTGCTATCTCCTGAATCT
GACAGGCAATGTGTTGATTTGGGGGTGGTAAGGGCTGATACCTGCATCAGACAGCCCTAT
GTACTTCTTTCTGGGTAACTGTCTGCCTAGAGATACTGCTCACTTCTGTCATCATTCCAA
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTGTGTCATGTATCACCCA
35 ATTCTATTTCTACTTCTTTCTCGGGGCTCCGAGTTCTTACTGTTGGCTGTCACTGTCTGGG
ATCGCTACCTGGCCATCTGTATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG
CTTTGCTGTGGCCTTGGCCTGCTGGGTGGGGGACTCGTCCCTGTGCTTGGTCCACAGTG
GCTGTGGCCTTGCTTCTCTTCTGTAAGCAGGGTGCTGTGGTACAGCACTTCTCTGCGCA
GTGGCCCACTGCTCCGCTGGCTTGCCACCAACCAAGAAGCTGGAGGAGACTGACTTTGT
CTCGGCTCCCTCTGTCATTTATCTTCTTGTGATCACTGCTGTGCTCTACGGCCCTATTG
40 TGCTGGCAGTCTGAGCATCCCTCTGCTCAGGCGTCAGAAGGCTTCTCTACCTGTAC
CTCCCACTTGATAGTGGTGACCCTCTTATGGAAGTGGCAATTTTCTCTATGTGCGGCCAT
CGCAGAGTGGTCTGTGGACCTAACTGGGCAAGTACAGTAATAACGACATTGTGACAC
CACTGTGGAATCCATTCATCTATGCCCTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
CATGTTTAGGAAGGTAGTGGCAGGCGTTTGAAGGAATCTTTACTTGATAAATGTCTCAGT
45 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

AOLFR79 sequences:

MTPGELALASGNHPTVTKFILQGSFNYPDLQELLFGAILLIYAITVVGNLGMMALIFTDSHLQSP
MYFFNLVLSFLDICYSVVTPKLLVNLVFLSDKSISFEGCVVQLAFFVVVHTAESFLLASMA YDR
50 FLAICQTHYGSIMTRGTCQLVAVSYAFGGANSALQGTGNVFLPFCGPNQLTHYCDIPLLH
LACANTATARVVLYVVSALVTLPAAVILTYSYCLVLVAIGRMRSVAGREKLDSTCASHFLAIAI
FYGTVVFTYVQPHGSTNNTNGQVSVFYTHIIPMLNPFIIYSLRNEVKYKALQRKLQVNIFFG
(SEQ ID NO: 147)

55 ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCAACCCAGTCACCAAGTTCATCT
TGCAGGGATTCTCCAATATCCAGACCTCCAGGAGCTTCTCTCGGAGCCATCTGCTCAT

ACAGCCGTGTGGCTGCTCTGCGCCGCTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
TGGATTTCCTGTGGGCCCAATGTCAATTATCCATTCTCTGCGAGGTCCCTCCCGTGTGCTT
CTCTCTGCGAGCTCCACCTACGTCAACGGTGTCAATGTTCTGCTGGCGGATGCTTCTACG
5 GCATAGTGAACCTCTGTATGACCATCGCGTCTCTATGGCTTCATGCTTCCAGCATCTGAA
GGTGAAGATGCTGCTGGGGGAGGAGAGAAAGCCTTCTCCACCTGTCTTCCACCTCACCGTG
GTGTGCATGTATTACACCGCTGTCTTCAACGCTACATAAGCCCGTCTCTGGCTACACGCG
CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGTGAGTCTTACCTCAACCCCT
CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTTCTTC
AGAAATTA (SEQ ID NO: 152)

10

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVFLRLYLGTLLGNLLIIISVKASQALKNPMFFFLFVLSL
SDTCLSTSIAPRMIVDALLKKTTSFSECMIQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII
SQWVCGVLMAVAVVWGCVHSLVQIFLALSLPFCGPNVINHCDFCLQPLLKQACMSEYTVVNNLL
15 VSNAGAICAVSYVMLIFSYVIFLHSLRNHSAEVIKKALSTCVSHIIVLFFGPIFYMTCPATVFP
MDKMIADVFTVGTSLNPVIYTLKNTEVKSAMRKLWSKLLITDDKR (SEQ ID NO: 153)

ATGCAACTGAATAATAATGTGACTGAGTTCACTTCTGCTTGGATTGACACAGGATCCTTTTT
20 GGAAGAAAATAGTGTTTGTATTTTTTTCGCTCTCTACTTGGGAACAACGTGTGGGTAATTT
GCTAATCAATTATAGTGCAAGGCCAGCCAGGCACCTAAGAACCCTAGTCTCTTCTCTCT
TCTACTATTCTTTATCTGATACTTGCCTCTCTACTTCCATAGCCCTAGAATGATTGTGGA
TGCCCTTTTGAAGAAGACAATATCTCTTCAACGAGTGATGATCCAAGTCTTTTTCATCC
CATGCTTTTGGCTGCTGGAGATCTTCACTCTCATCTCAGCCTGATGACCGCTATGTGGA
CATCTGTGAAGCCCTGCACTACATGACCATCATAAAGCAGTGGGTCTGTGGTGTITGTATG
25 GCTGTGGCTGGGTGGGATCCTGTGTGCACTTCTTTAGTTAGATTTTCTTGCCCTGAGTTT
GCCATTCTGTGGCCCAATGTGATCAATCACTGTTTCTGTGACTTGACGCCCTTGTGAAA
CAAGCCTGTTCAGAAACCTATGTGGTTAACTACTCTCTGTTTCCAATAGTGGGCCATTT
GTGCAAGTGTGATGTGCAATGCTAATATCTCTACTGTCTTCTGTGATCTCTGAGAAAC
30 CACAGTGTGAAAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCATTTGTGGTCA
TCTGTCTTGTGAGCTTGATATTTATGACATGCGCTGACCCATTCACCCGTAATCCCATGGAT
AAGATGATAGCTGTATTTATACAGTTGGAACATCTTTCTCAACCTGTGATTTACACGCT
GAAGAAATCAGAAGTGAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATGATCAGAGA
TGACAAAAGATA (SEQ ID NO: 154)

AOLFR83 sequences:

MGNWTAAVTEFVLLGFLSREVELLLLVLPTFLLTLLGNLLIISTVLSCSRHTPMYFFLCNL
SILDILFTSVISPKVLANLGSRDKTISFAGCTQCYFYFFLGTIVFELLTVMISYDRYATICPLRYT
TIMRPSVCIQTVVSVWVGFLSVLFTILISQLPFGCSNIINHFCDSGPLLALACADTTAIELMDP
15 MLSMVLICCVLVAYSYTYIITVIRIPASGRKKAFTNCASHLTIIVIPSGITVFYIVTPSQKEYL
EINKPLVLSVVTFPLNPFYITLRNDTVQGVLRDWWVRVGVFEKMRVLRSLSSNKDHQ
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

ATGGGTAACTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCTGAGCAGGG
45 AGGTGGAGCTGTGCTCTGCTGCTGCTGCTGCCACGTTCTGCTGACTCTTCTGGGGAA
CCTGCTCATCATCTCCACTGTGCTGCTCTTCACTTCACTCAGTCATCTTCCAAAAGTGTGGCC
AACTTAGGATCTAGGAGATAAAACATCTCTTTCGCGGATGATACACCCAGTGCTATTTCT
ACTTTTCTTGGGACAGTTGAGTTCTCTGCTGACGCGTATGCTTATGACCGTTATGCG
ACCATCTGCTGCCCGTGGCGTACACCATCATGAGACCTTCTGTGCAATGGGACCG
50 TGTATTCTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTCCAAACCATCCTCATCTCCAG
CTGCCCTTCTGTGGCTCCAATATCATTAACCACTTCTTGTGACAGTGGAACCTTGTGGC
CCTGGCCTGTGCAGACCACTGCCATCGAGCTGATGGATTTATGCTTTCTTCCATGGTC
ATCTCTGTGTCATAGTCTGCTGGCCATTCCTATCTATACGTACATCATCTTGACCATAGTGCG
CATTCCTTCTGCAAGTGAAGGAAGAAAGGCCTTAATACCTGTGCTTCCACCTGACCATCA
55 GTCATCATCTTGTGAGTGGCATCACTGTGTTTATCATCTGTGACCTCCCAAGAAAGATATCT
GGAGATCAACAAGATCCCTTGGTCTGAGCAGTGTGGTGACTCCATCTCTCAACCCCTTT

ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCCCTCAGGGATGTGTGGGTCAGGGTT
CGAGGAGTTTTTGAAGAGGATGAGGGCAGTGCTGAGAGCAGATTATCTCCAAACAA
GACCAACGAAGGAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGT
AG (SEQ ID NO: 156)

5

AOLFR85 sequences:

MGAKNNVTEFVLGFLFESREMQHTCFVVFLLFHVLTVLGNLLVIITNARKTLKSPMYFFLSQL
SFADICYPSTTIKPMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRCKGLLAGASWLAGFLHSILQTLTLTVQLPCFGCPNEIDNFFCDVHPLLLKACADTYMV
GLIVVANSGMISLASFFILIISVVIILLNLRSSQSEDRRAVSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLILFNIVMPPLLNLPLYTLRNNDVKNAMRKLFRVKRSLGK (SEQ ID NO: 157)

10

ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTATTTGGCCTTTTGTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCTCTCTTTCATGTGCTCACTGTCTGGGGAAACCTT
CTGGTCATCATCACCATTCAATGCTAGAAAGACCTGAAGTCTCCCATGTATTCTTCTCTGAG
GCCAGTTGTCTTTTGTGACATATGTTATCCATCCATACCACCAAGATGATTTGCTGAC
ACTTTTGTGAGCATAAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTCTGCCCCA
CTTCTTTGGTGGCAGATCTTCTCTCTTACAGCCATGGCCTATGACCGCTATGTGGCC
ATCTGTAGGCCCTTGCATCACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
GGGCTCTGTGTTAGCTGGCTTCTGCAATCCATCTGTCAGAGCCCTCTCACGGTTACAGCTG
CTTTTGTGGGGCCCAATGAGATAGACAACTCTCTGTGATGTTTCATCCCTGCTCAAGTT
GGCTGTGACAGACCTACATGGTAGGTCTCATCGTGGTGCCCAACACGGGTATGATTCT
TTAGCATCTTTTATCTCTTATCATTTTCTATGTTATCATCTTACTGAACCTAAGAACGCA
GTATCTGAGGACCGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCTCTT
TGTGTTCTCATGCCCCCATGTTTCATGTACATTCGTCCTCCACACCTCCAGCTGCTGACAA
ACITATCATCTCTTTAACATTGTGATGCCACCTTTGCTGAACCCCTTGTATCTATACACTAA
GGAACACGATGTAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
AGAAGTGA (SEQ ID NO: 158)

20

25

30

AOLFR86 sequences:

MLVLLMLFLLVFIGNTAPAFSVTLSEMDIPQNITEFMLGLSQNSEVQRVLVVFLLIYVVTVC
GNMLIVVTTSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECMCMAQLFGAHP
LGGVEIILLTVMAYDRYVAICKPLHNTTMRHLKAMLVGVAWLGGFLHLSLVQLLLVWLWLPFC
GPNVINHFACDLYPLEVACINTYVIGLLVAVNSGLICLLNFMILAAASYVILYSLRSHSADGRC
KALSTCGAHFIVVAFVPCIFIFYVHPFSTLPIDKNMALFYGILTPMLNPLYTLRNNEEVKNAMR
KLFTW (SEQ ID NO: 159)

35

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
CTCAGTGACCTTGGAAATCTATGGACATACCACAAAAATATCACAGAAATTTTTCATGCTGGGG
CTCTCAGAACTCAGAGGTACAGAGAGTCTCTTTGTGGTCTTTTGTGATCTATGTGG
TCACGGTTTGTGGCAACATGCTCATTTGTGGTCACTACCTCCACGCCACCGCTGGCTTC
CCCTGTGATTTTCTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTCTTCTATGGC
TCTAAACTCATGCTGACTCATTGTATGAGGGGAGAACCATCTTATGTAGTGCTGCATGT
GCTCAGCTCTTTGGAGCTCATTTTGTGGGAGGTGTTGAGATCACTTCGTCACAGTGATGG
CTTATGACCGCTATGTGGCCATCTGAAGCCCTGCACAATACTACCATCATGACCAGGCA
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTCGATTCAATTGGTTCAG
CTCCTCTGTGCTCTTTGGTTCGCCCTTCTGTGGGCCCAATGTGATCAATCACTTGTGCTGTGA
CTTGTACCCCTTTGTGCGAAGTTTGCTGCACCAATACGATATGCTTGGCTGCTGGTGGT
GCCACAGTGGTTTAACTGCTGTTTGAACCTTCTCATGCTGGCTGCCCTCACTATGTGAT
CTCTGATCTCTGAGGTGCCACAGTGCAGATGAGATGAAGGCCCTTCCACCTGTGGA
GCCACCTTCATTGTTGTGCTTGTCTTGTGCCCTGTATATTACTTATGTGATCCATTT
TCTACTTTACCTATAGACAAAAATATGGCATTATTTATGGTATTTGACACCTATGTTGAA
TCCACTCATTTATACCTGAGAAATGAAGAGGTAAAAATGCCATGAGAAAGCTCTTAC
TGTGTA (SEQ ID NO: 160)

55

AOLFR87 sequences:

- MMNIAQSLGFDLGPISVLQKILTKIILLFKMYVSNCPCAIHRKINYPNTKLDFEQVNNITEFI
LLGLTQNAEAKQLFLAVFTLIYFLTMVDNLIIVVTTITSPALDSPVYFLSFFSFDGSSSTMAP
KMIFFDLLTEKKTISFSGCMTQLFVEHFFGGVEILLVVMAYDCYVAICKPLYLITMNRQVCGL
LVAMAVWVGFLHALQMLLIWLPFCGPNVIDHFICDLFPLKLSCTDTHVFLGVFAANSGLM
CMLIFSILITSYVLLILCSQRKALSTCAFHITVVVLFVFPCLVYLRLPMITFPIDKAVSVFYTVTPM
LNPLIYTLRNTVEKNAMKQLWSQIHWGNLCLD (SEQ ID NO: 161)
- 10 ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTAGGGATTCCATCAGTGTAC
AGAAAAATCTGTGACCAAAATATTTTATTGTTCAAAATGATGTGTCAAATGCAATCC
TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAACTGGATTTCGAGCAAGTGAAAC
AACATAACGGAAATTCATCTTGCTTGGCCTGACACAGAAGCGAGAGGCACAGAACTCTTGT
TTGCTGTGTTTACACTCATCTACTTTCTACCATGGTAGACAACCTAATCAATTGTGGTGACA
ATCACCACAGCCAGCCAGCCTGGACTCCCCCGGTGATTTTTTCTGTCTTTCTTTCTCTCAT
15 AGATGCTGTCTCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAG
AAAACTATTTCCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTCTTCTTGGGGGAG
TTGAGATCATCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCT
GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCGTGGGCCATGGCATGGGTG
GGGGGATTCTTTCAGCTCTGATTCAAAATGCTTTAATAGTCTGGCTGCCCTCTGTGGCCC
20 CAATGTCTATGACCATTTCTCTGTGACCTTTTCCCTCTGCTAAAACTCTCTGCACTGACA
CTCAGCTCTTTGGAATCTTTGTTGCCGCCAACAGTGGGCTGATGTGATGCTCATTTTTCT
ATTCTATTACCTCTACGTCTTAATCCTCTGCTCACAGCGGAAGGCTCTCTACTGCGC
CTTCCATATCACTGTAGTCGTCTATTCTTTGTTCCTGTATATTGGTGTACCTTCGACCCA
TGATCACCTTCCCTATGTATAAAGCTGTGTCTGTGTTTATACTGTGGTAACACCCATGTTA
25 AACCTTTAATCTACCCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

- MWQKNQTSLADFILEGLFDDSLTHLFLSFLTMVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
LSLMDLMHVSTIILKMATNYLSGKKISISFVGCAQTQHFLYLCLGGAEFCFLAVMSYDRYVAICH
PLRYAVLMMNKKVGLMMAVMSWLGASVNSLIHMAILMHFFPCGPRKRVYHFYCEFPVAVKLV
GDITVYETTVYISSILLPLIFLISTSYVFIQSVIQMRSSGSKRNAFATCGSHLTVSVLWFGACIFS
YMRPRSQCILLQNKVGSVFYSIITPLNSLIYTLRNKIDVAKALRRVLRRDVITQICRIQLWL
RV (SEQ ID NO: 163)
- 30 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
CCCTTACCCACCTTTCTCTTTCTCTCTTGACCATGGTGGTCTTCTTATTGCGGTGAGTGGC
AACACCCCTACCATTTCTCCCTCATCTGCATTTGATCCCCAGCTTCATACCAATGATTTCCT
GCTCAGCCAGCTCTCCCTCATGGAATCTGATGCATGTCTCCACATCATCTCAAGATGGCT
40 ACCAATACCTATCTGCGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCGACACTTCC
TCTATTGTGTCTAGGTGGTGTCTGAATGTTTCTCTTAGCTGTCTATGTCCTATGACCGCTAT
GTTGCCATCTGTCATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGTGGGACTGATGA
TGGCTGTCATGTCTATGTTGGGGGCAATCCGTGAACCTCCTAATTCACATGGCGATCTTGT
GCACTCTCCCTTTCTGTGGGCTCGGAAAGTCTACCACTTCTACTGTGAGTTCACAGCTGTTG
45 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCAGGTACATCAGCAGCATCTCT
CCTCCTCTCCCATCTTCTCTGATTCTACATCCTATGTCTCTATCCTCTCAAGAGTGATCTCA
GATCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCACTGTGGCTCCCACTCAAGCTGCGG
GTTTCTCTTTGGTGGTGCCTGCATCTTCTCTCATGAGACCCAGGTCCCAGTGCATCT
ATTGCAACAACAAATTTGGTTCTGTGTTCTACAGCATCATTACGCCCACTTGAATTTCTGT
50 ATTTATACTCTCGGAATAAAGATGTAGTAAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
GTTATACCCAGTGCATTACACGACTGCAATTGTGGTGTGCCCGAGTGTAG (SEQ ID NO:
164)

AOLFR89 sequences:

- 55 MLDPSISHTLYLHSLFPQLRKGTMTWQKNQTSLADFILEGLFDDSLTHLFLSFLTMVFLIAVS
GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTIILKMATNYLSGKKISISFVGCAQTQHFLYL

CLGGAECFLLVAMSYDTRYVAICHPLRYAVLMNKKVGLMMAVMSWLGVASVNSLIHMAILMHF
PFCGRKRVYHYFKCEFPVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILOSQVIMRSSGSK
RNAFATCGSHLTIVVSLWFGACIFSYMRPRSQCCTLQNKVGSVFYSIITPLNSLIYTLRNKDVA
KALRRVLRRDVTIQCIQRLQLWLPV (SEQ ID NO: 165)

5 ATGCTGGACCCAGTATTTCAGTCACACTCTTTATCTCCACTCTCTGTTTCTCAGGGATT
GAGAAAGGGGACAAATGTGGCAGAGAATCAGACCTCTCTGGCAGACTTCATCTTGAGGG
GCTCTTCGATGACTCCCTTACCCACCTTTTCCTTTTCTCCTTGACCATGGTGGTCTTCCTTAT
10 TGCGGTGAGTGGCAACACCTCACCATTCTCCTCATCTGCATTGATCCCGAGCTTACATACA
CAAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
ACCCAGCACTTCCCTCTATTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCAATGTC
CTATGACCGCTATGTTGCCATCTGTCTATCCACTGGCCTATGCTGTGCTCATGAACAAGAAG
GTGGGACTGATGATGGCTGTCTATGTCTGTTGGGGCATCCGTGAACCTCCCTAATTACACA
15 TGGCGATCTTGATGCACCTTCCCTTTCTGTGGGCCCTGGAAAGTCTACCATCTTACTGTGA
GTCTCCAGCTTGTGGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
ATCAGCAGCAATTCTCTCTCTCCCTCCCATCTTCTGATTCTTACATCGTATGCTTCTCATCTCT
CAAAAGTGTCATTAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG
20 TCCAGTGCACCTTATTGTCAGAAACAAAGTTGGTCTGTGTTCTACAGCATCTTACGCCCA
CATTGAATTTCTGATTATTACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
GCTGAGGAGATGTTATCACCCAGTGCAATCAACGACTGCAATTTGGTTGCCCGGAGTG
TAG (SEQ ID NO: 166)

25 **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAIFISLGNMQNQSFVTEF
VLGLLSONPNVQEIFVFLVFLVYIATVGGNMLIVVTLLSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKIMVDSLTVYTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRLL
CGILMGVAWTGGLLHSMIQLFTTQLPCFPNPNVHFMCDLYPLLELACTDTHIFGLMVVINSF
30 FICINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVILFFVPCIFVYTRPPSAISLDKMA
AIFYIILNPLLNPLYITFRNKVEVKQAMRRIWNRLMVVSEKENIKL (SEQ ID NO: 167)

ATGTCTCAATGACAACAGAAGCACTCAATAATTTGCACTTGGATGTACCAACTTGTTAA
TGACTATGATACCCAAATGATCTGAAGCAAAATTTCTTTGTCCTAATTGCAGACATATA
35 CATGATCCCTGTTGGAGCTTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCTCTGGGACITTCACAGAATCAAATGTTTCAGGAAATAGTATTGTGT
TATTTTTGTTGTCTACTGCAACTGTGGGGGGCAACATGCTAATTGTAGTAAACCAATCTC
AGCAGCCCTGCCTCTCTGTTGTCTCCTATGTACTTCTTCTGGGCTTCTGCTCTCTCGGA
40 TGCGTGCTTCTCATCTGTGATACCCCAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTCTTTTGTCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TTACTCTTCTACTGAACAGGAGGCTCTGTGGCAITCTGATGGGGTCTGCTGGCAGGG
GGCCTCTGTGATTCATGATACAAATCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCTGCACTGATACTC
45 ACATCTTTGGCCTCATGGTGGTCAACAGTGGGTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTTGTCTCTGTGAGAACACAGTTCTGGAAGGGGCGTG
GAAAGCTCTCCACCTCTGGGATCTCACATTGCTGTGATTGTTGTTCTTTGTCCCATGCA
TATTTGTATATACAGCACTCCATCTGCTTTTTCCTTGACAAAATGGCGGCAATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTTACACTTACGAAATAAGGAAGTAAAC
50 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

MDNWSTVTEITLAPFALLEIRISLFFVLVVTYTLTATGNITISLIWIDHRLQTPMYFFLSNLSFL
55 DLYTTVTIPKLALCLGEEKTISFAGCMQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI
MNSRACLNLVLGCWVGAFLSVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFL

098605.06201

SALVILSSLAFTTGSVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
YDKVA AVLITVVTPLLNPFYISLRNEKVQEVLR ETVNRIMTLQRKT (SEQ ID NO: 169)

ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA
5 TCGGAATATCTCTCTCGTGGTCTTGTGGTAACCTACACATTAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACTCCAATGTACTCTTCCTCA
GTAATTGTCTCTTCTGGATATCTTATACACCACTGTCAATACCCCAAAGTGTGTGGCCTGC
CTCCTAGGAGAAGAGAAACCATATCTTTGTCTGGTGCATGATCCAAACATATTTCTACT
10 TCTTTCTGGGGACGGTGGAGTTATCTCTTGTGGCGGTGATGTCCTTTGACCGCTACATGGC
TATCTGCGACCCACTGCATACACGGTCATCATGAACAGCAGGGCTGCCCTCTGTGCGTT
CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTGTGTTCCAAACCATTTGATAGTGACAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTTCTTCTGTGACATTTGCCCTCTCTTTCAGGTG
GCCTGTATAAAATACCTCACTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTGTGCTCCT
15 GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAAATTTCTACCATCTCGGTATCC
CCTCCACCCAGGGCCGTGAGAAAGCTTTTTCTACCTGTGCTTCTCATCATCACTGTTGTCTCC
ATGTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCTCACTGGATT
ATGACAAGGTGGCGCTGTCTCATCACAGTGGTGACCCCTCTCTGAACCACTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGCAATCTGAC
20 CTTGATACAAAGGAAACCTTGA (SEQ ID NO: 170)

AOLFR92 sequences:

MRNGTVITEHLLGFPVIQGLQTLPLFIAIFLYILTLAGNLIATVWAEPLRQIPMYFFLCNLSFLE
IWYITTVPKLLGTFVAVARTVICMSCLLQAFHFFVGTTEFLITIMSFDRYLITCNPLHHPTIM
TSKLCLQALSSWVVGFTIVFCQTMILLIQLPFCGNVNSHFVCDVGPBLSKAAACIDTSILELLGVA
25 TILVPSGLLNMISYIYLISAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVSVLNTILTPLLNPFYITIRNKEVKGLRKMTCPKTGHA (SEQ ID NO: 171)

ATGAGAAATGGCACAGTAATCAGAAATCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCCCTTGACGGAATGGG
30 CTTATTATTGCCACTGTGTGGGCTGAGCCAGGCTGACAAATCCAATGTACTCTCTCTTGT
TAACCTGTCTTCTTAGAAATCTGGTACACCCACAGTCATCCCCAAACCTGCTAGGAACC
TTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCCCTGCTGCAAGGCCCTCTTCCACT
TCTTCGTGGGCACCAACCGAGTTCTTGATCCTCACTATCATGTCTTTTGACCGCTACCTCAC
ATCTGCAATCCCTTCTACCCACCCACCATCATGACACGAAACTCTGCTGTCGACGCGCC
35 TGAGCTCCTGGGTGGTGGGCTTCAACATTGCTTTTGTGACAGCATGCTGCTCATCTAGTT
GCCATCTGTGGCAATAATGTTATCAGTCATTCTACTGTGATGTTGGGCCCAGTTTGAAA
GCCGCTGCATAGACACCAAGCATTTTGAAGCTCCTGGGCGTCATAGCAACCATCTTGTGA
TCCCAAGGTCACTCTCTTTAATATGATTTCTATATCTACATCTGCTGCCGAATCTCACA
ATTCTCTCAGCCACTGGCCACCAAAAGACTTTCTACTCTGTGCTCGACCTGACAGTTGT
40 CTCTCTGCTCATCGGGCTGTCTGTTCATGTACCTAAGACCCACGACACTCTCCTCTTA
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCTCCTACCCCTCTTGAATCCCTTTATT
TATACTATTAGAAACAGGAGGTGAAGGAGCCTTAAGAAAGCAATGACTTGCCCAAAG
ACTGTCATGCAAAGTAA (SEQ ID NO: 172)

AOLFR93 sequences:

MLMNYSSATEFYLLGFPGEELHHLFAIFFFYLVTLMGNTVIMIVCVDKRLQSPMYFFLGH
SALEILVTTIVPVMWGLLLPGMQITYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIMNRHTCNFVVLVSVVFGFLQIWPVYVMFQLTICKSNVNNFFCDRGQLKLSCN
NLFTEFILFLMAVFLVGLSLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY
55 VKPQKTQADYNWVSLMVSVVTPFLNPFIFLRNDKVI EALRDGVKRCCQLFRN (SEQ ID
NO: 173)

ATGTTGATGAATTACTCTAGTGCCACTGAATTTATCTCCTTGGCTCTCCCTGGCTCTGAAGA
ACTACATCATATCTCTTTTGTATATTTCTCTTTTCTACTTGGTGACATTAATGGGAAACA
60 CAGTCATCATATGATGTCTGTGTGGATAACGCTGCGAGTCCCCCATGTATTTCTCTCT
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAAACCAATCTGCCCTGTGATGCTTTGGG

5 GATTGCTGCTCCGTGGGATGCAGACAATATATTGTCTGCTGTGTGTGCCAGCTCTTCTTG
TACCTTGCTGTGGGGACAACAGAGTTCGCAATCTATTGGAGCAATGGCTGTGCCCGGTATG
TGGCTGTCTGTAACCCCTCTGAGGTACCAACATCAATTGAACAGACACACCTTGCAACTTGT
GGTTCTGTGTCACTGGGTTGTGGGTTTGGTTTGTTCCTTCAAATCGGCCGGCTATGTCAATGTT
AGCTTACTTACGAAATCAAATGGTGTGTAACAATTTTGTGTACCGGAGGCAATGCT
TAACTACTCTCGCAATAATCACTTTTCAGGAGTTATCTCTCTCTTAATGGCTGTGTTT
10 CTTCTTTGGTCTTTGATCCCTCAATTTTCACGAGCCCTACATCTCCACCATCTC
AAGATCCCGTCACTCTCTGGCCGGAGGAAATCTCTCCACTTGTGCTCTCCACTTCAACCTG
TGTGTGTGAATGGCTACCGGCGAGGTAATCTCTCTACGTGAAACCAGCAACCGCAGGCA
GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACCTCTTCTCAATCACTT
CATCTCCACCTCCGGAATGATAAGCTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
TGCAACTATTACGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

15 METWVNQSYTDGFFLLGIFSHSTADLVLFVSVMVAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
LSQLSMDLMDLVCTNVPKMAANFLSGKISFVGGCGIGLFVCLVSGEGLLGLMAYDRYVA
ISPHLHYPLMNQRCVLQITGSSWAFGLIDGLQMVVMNFPFYCGLRKVRNHFFCEMLSLKLKAC
VDTSLFEKVIFACCVFMLLPFSIIIVASYAHILGTVLQMHSQAQWKKALATCSSHLTAVTLFYG
AAMFTILRPRIYAPSHDKVASIFYTVLTPMLNPLIYSLRNRREVGMALRKLGLDRCRIGSQH
20 (SEQ ID NO: 175)

25 ATGGAGACGTGGGTGAACCACTCTACACAGATGGCTCTCTCCCTCTTAGGCATCTCTCC
ACAGTCTGCTGACAGTCTGCTCTCTCTCTGAGTGTATGGCGGTCTACAGATGGCCCTCTGT
GGAAATGCTCTCTCTCATCTTCTCATCTACATGGACCTCACTTCAACCCCCATGTACT
CTTCTCTCAGGCAGCTCTCCCTCATGGACTCATGTGGTCTGTACCAATGTGCCAAAGATG
CGACGCCAATCTCTGTCTGGCAGGAAGTCCATCTCTTGTGGGCTGTGGCATACAAATG
GCCTCTTGTCTGTCTTGTGGGATCTAGGGGCTCTTGTGGGACTGAGCTTATGACCG
CTATGTGGCCATAGGACCCACTTCATATCCCATCTCTATGAATCAGAGGGTCTGTCTCC
AGATTACTGGAGACTCTCTGGGCTTTGGGATAATCGATGGCTTGAACCAATGTGTGGTAGT
30 AATGAATTTCCCTTACTGTGGCTTGAGGAAGGTGACCAATTTCTTCTGTGAGATGCTATCC
TTGTTGAAGCTGGCCCTGTGATGACACATCCCTGTTTGAAGAAGGTGATATTTGCTTGTGTG
TCTTCATGCTTCTTCTCCCAATCTCATCATCTGTGGCTCTATGCTACATCTAGGACT
GTGCTGCAAAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCTCTCCACC
TGACAGCTGTACCCCTCTCTATGGGGACAGGATGTCTACTCTACAGGCTTAGGCCATAGGCACTA
35 CCGGGCCCCAGCCATGACAAGGTGGCTCTATCTCTACACGGTCTTACTCCCATGCTC
AACCCTCATTTATACAGCTTGAGGAACAGGGAGGTGATGGGGGCTAGGGAAGGGGCTG
GACCGCTGACAGGATCGGCAGCCAGCTGAA (SEQ ID NO: 176)

AOLFR95 sequences:

40 MLGSKPRVHLYILPCASQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILFLFLFVYAMILL
GNVGMMTIMTDPLRNTIPMYFLNLISFDILFYSSVEPKAMINFWSCNSISFAGVCVQLFLFA
LIVTEGELLAAAYDRFIAICNPLLYSVQMSRTRLQVLGVSFGCGISSVYITQSMITFLSFLCAS
RAVDHFYFCDSRPLQRLSCSDLFHIRMISFSLSCIIILPTIIVIVSYMYTVSTVLKIHSTEGHKKAFST
CSSHLGVVSVLYGAVFMFMYLTPDRFPELSKVASLCSYLVTPMLNPLIYSLRNKDVQEALKKFLE
45 KKNIL (SEQ ID NO: 177)

50 ATGCTAGGATCCAAACCAAGAGTTCAATTGTATAATTTGCGCCTGTGCCCTCAACAGGTTTC
TACCATGGGTGACAGGGGAACCAAGCAATCACTCAGAAATGACTGACTCATCTTCGAGGC
CTTCAGGGTACGCCAGAGCTCCACATCTCTCTCTGTAATTTTGTGTGTTATTGCCA
TGATCCTCTTAGGGAATTTGTGGGATGATGACCAATTAATGACTGATCTCGGCTGAACAC
ACCAATGATTTTCTTAGGCAATCTCCTCAATGATCTTTTATTCATCTGTTATTGTA
ACCCAAGGCTATGATCAACTCTCGGTCTGAAACAAAGTCTATATCTGACAGGCTGTGIG
GCCAGCTCTTCTTTCTGGCCCTCAATCTGACTGAGGAAATTCCTCTGGCGGCCATGGC
55 TTATGACCGCTTTATTGCCATCTGCAACCCCTGCTCTACTCTGTCAAATGGTCAACAGCT
TGTTGACTCAGTTGGTGCGTGGTTCCTAATTTTGTGGCTGCATAGCTCAGTTATTCAGCA
AGCATGACATTTACTTATCTTTTGGCGTCTCTCGGGCTGTGACCACTTTTACTGTGATTC

TCGCCCACTTCAGAGACTGCTTGTCTGATCTCTTATCCATAGAATGATATCTTTTTCCT
TATCATGTATTATTATCTTGCTACTATCATAGTCAATTATAGTATCTTACATGTATATTGTG
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTGCTCTTTTATGTATCTCACTCCTGAC
AGATTTCCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCTAGTCACTCCCATGTGTA
ATCCTTTGATTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAAATTTCTAGA
GAAGAAAAATATTATTCTTGA (SEQ ID NO: 178)

AOLF96 sequences:

- 10 MICENHTRVTEFILLGTFTNNPEMQVSLFIFFLAIYTVTLGNFLIVTVSDVLAQLTPMYFFLQN
LSLLEVCFVLVMVPMKMLVDLVSPRKIIISFVCGCTQMYFFFFGSSECFLLSMMAVDRFVAICNP
LHYSVIMNRSCLLWMAIGSWMSGVPVMSLQTAWMMALPFCGPNAVDFHFFCDGPPVLKLVTV
DTTMYEMQALASTLLFIMFPCLILVSYTRIHTILRMSSATGRQKAFSTCSSHLLVLSLFGYTASL
TYLRPKNSQSPESKKLVSLSYVITPMLNPIHGLRNNNEVKGAVKRITITQKVLQKLDVF (SEQ
ID NO: 179)

- 20 ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATCTTCTTGGTTTTACAACAACCC
CCGAGATGCAAGTTTCCCTCTTTATTTTTTCTTGCCCAATTTATACAGTCACTTTGTTGGGC
AACITTTCTTATTGTCACAGTACCAGTGTGGATCTCGCATCTCAAAACACCCATGTACTTCTT
TCTTCAAAATCTGCTCACTTCTTGAAGTATGTTTACCTTGGTATGGTGCCAAAAATGCTTG
TAGATCTAGTGTCCCAAGGAAAAATTATCTCTTTTGTGGGCTGTGGTACCAGATGTACTT
CTTCTCTCTCTTTGGCAGTTCTGAATGTTTCTCTCTCCATGATGGCTTATGATCGGTTTGT
GGCCATCTGTAAACCTCTCCATTATTCACTCATAAATGAACAGGTCCTATGCTGTGGATG
GCCATAGGCTCTTGGATGTCGGGTGTTCTGTGCTATGTCTACAGACAGCTTGGATGATGG
CCCTTCTCTTCTGTGGACCAATGCCGTGGACCACTTTTCTGTGATGGTCCCCCAGTGTAA
AACTAGTCAAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT
TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCAATCTATCAACAATCTGT
AGGATGTCTCTGCCACTGGCCGCCAGAAGGCATTTCTACTTGTCTCACACCTTACTGT
GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACTCGGGGCCAAATCAAACAGGATCC
30 CTGAGAGCAAGAAGCTAGTGTCTATTGCTCTACACTGTCAACACTGTCTCAACCCCA
TCATCTACGGGCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAA
AAGCTTACAGAAGTTAGATGTGTTTGA (SEQ ID NO: 180)

AOLF97 sequences:

- 35 MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSFMVVPSFSIAEHWRMRKGANLSQGMFEL
LGLTTDPQLQRLFLVFLGMYTATLLGNLVMFLIHVSATLHTPMYSLKLSFLDFCYSSSTV
PQTLVNLAKRKYVIFGCMTQMFFYAGFATSECYLIAAMAYDRYAIAICNPLLYSTIMSPEVC
ASLVGYSYAGFLNSLHYTGICFLKFCGAAHVVTTHFFCDGPPILSLCVDSTSLCEILLFIAGFNLLS
CTLTILISYFLILNTILKMSSAQGRFAFSTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRIVA
40 VIYTVVIVPLNPLMYSRLNKDVKKALIKVWGRKTIME (SEQ ID NO: 181)

- 45 ATGACAGAGTTTCACTCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
CCTTAGGACAGAATTAACCCAGTCAAGGCCCAAGGTGTTCAACCTCATTTATGGTGGTGCC
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAACCTGAGCCAAAGGAT
GGAGTTTGAGCTTCTGGGCTCACCACCTGACCCCAAGCTCCAGAGGCTGCTCTTCTGTGGT
TTCTGGGCATGTACACAGCACTCTGTGGGGAACCTGGTCATGTTCTCTGATCCATG
TGAGTGCCACCTCGACACACCATGTACTCCCTCTGAAGAGCCCTCTCTTCTTGGATTTCT
TGCTACTCCTCCACGGTTGTGCCCAAGACCCTGGTGAACCTTCTGGCGTAGACAGCAAGATGA
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCCGGGTTTGGCACCACTGAGTGC
50 TATCTCATGGCTGCCATGGCCTATGACCGCTATGCCGCTATTTGTAACCCCTGCTCTACTC
AACCATCATGCTCTCCTGAGGCTGTGCGCTCGTGATTGTGGGCTCTACAGTGCAGGATTCT
CTCAATTCTCTTATCCACACTGGCTGTATCTTATGCTGAAATCTGCGGTGTCTATGTCGT
CACTCACTTCTTCTGTGATGGGCCACCATCCTGTCTTGTCTGTGTACACACCTCACTGT
GTGAGATCTGCTCTTCAATTTTGTGTTTCAACCTTTTGTGAGTGCACCTCACTCATCTGT
55 ATCTCCTACTCTTAATCTCAACACCATCCTGAAATGAGCTCGGCCAGGGCAGGTTA
AGGCATTTTCCACCTGTGATCCACCTCACTGCCATCTGCTCTTCTTGGCACAACTT

00000000000000000000

5

10

15

30

30

40

55

LVDFVINSCKILATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK
KSYSLDYDQALAVVYSVLTPLFNFFIYSLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

5 ATGGACACAGGGAAGCTGGAGCCAGGTAGCAGAATTCATCATCTTTGGGCTTCCCCCATCTCC
AGGGTGTCACGATTATTCCTCTCTCTGTGCTCTCATTTACCTCATGACTGTGTGGGA
AACTCGTCAATTTCTGGTGGTCTGCCTGGACTCCCGGCTTACACACCAATTCCTGATCA
TTGTCAGCATCTCTCCTCTCTCAGAGCTTGGGTATACAGCTGCCACCACTCCCTAAGATGCTG
GCAAACTTGCTCAGTGAGAAAAAGACCAATTTCACTCTGGGTGTCTCCTGGCAGATCTATT
TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCCTACGATAGGTA
10 TTTAGCCATCTGCGCGCCCTCCACTACCAACCTCATGACCCCAACTTTGTGCAGAG
ATTGCCATTGGCTGTGTGGTGGGAGGCTTGGCTGGGCCAGTAGITGAATTCCTTGATTT
CAGCGCTCCCAATTCGTGGCCCCAATCGCATTCAGCAGCTCTTTGTGACTTCCCTCCTGTG
CTGAGTTGGCTTGCACGTGATACGTCTATAAATGTCTAGTAGATTTTGTATAAATTCCTG
CAAGATCCTAGCCACCTTCTGTGCTGATCCTCTGCTCCTATGTGCAGATCATTCGACAGTGC
15 TCAGAATTCCTCAGCTGCCGCAAGAGGAAGGCCATCTCCACGTGTGCCCTCCCACTTCA
TGTGGTTCTCATCTTCTATGGGAGCATCCTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
TCACTGGACTATGACCAGGCCCTGGCAGTGGTCTACTCAGTGTCTACACCCCTCCTCAACC
CCTCATCTACAGCTTGCACAACAAGGAGATCAAGGAGGCTGTGAGGAGGCACTAAAGA
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

20
AOLFR102 sequences:

MPVGGKLVFNQSEPTFVFRAFTTATEFQVLLFLLFLLLYLMILCGNTAIWVVCVTHSLRTPMYF
FLNSLSELECYTTVVVPLMLSNLGAQKPSLGAQGMFFVLTGSTDCLLAIMAYDRYVAI
CHPLHYLTIMTRELCTQMLGGALGLALFPLSLQ.TALIFLTPFCGHHQHEINHLFCDPVYLRLACA
25 DIRVHQVLYVVVLSILVTIPFLLCVSYVFTTCILRSABEGRRRAFSTCSFHLTVLLVPLGCCSL
VYLRPRSSTSEDEDSQIALVYTFVTPLNPLLYSLRNKDVKGALRSAIRKAASDAN (SEQ ID
NO: 189)

30 ATGCCTGTGGGAAACTTGTCTCAACCACTGTGAGCCCACTGAGTTGTGTTCCTGGCT
TCACCACAGCCACTGAATTCAGGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
ATCCTCTGTGCCAACACAGCCATCATCTGGGTGGTGTGTCACACACAGCACCCTCCGACCC
CGATGTATTTCTCTCTGTCACCACTGTCTTCTCTGGAACCTGTGTACACCACTGGTGTAGTA
CCTTGATGCTTTCCAACATTTGGGGGCCCAAGAAGCCATTTCTGTGGCTGGATGTGGGG
35 CCCAAATGTTCTCTTTGTACCCCTCGGCAGCAGGACTGTTCTCTCTGTGGCGATCATGGCC
TATGACCGCTATGTGGCTATCTGCCACCCGCTGCACTACCCCTCATGACCCGCGAGC
TGTGCAACGAGATGCTGGGTGGGGCCCTGGGCCTGGCCCTCTCCCTCCCTGCAGCTCAC
CGCCTTAATCTTCAACCCTGCCCTTTTGGGGCCCAACAGGAATCAACCACTTCTCTGCG
ATGTGCTCTCCGTCCTGCGCTGCGCTGCGCTGACATCCGCTGACACGAGCTGTCTCTCA
TGCTGTGAGCATCTCTGTGCTGACCATCCCTCTCTGTCTCATCTGCTCTCTCACTGTGCTCA
40 TCACTGTGGCATCTCTGAGCATCCGTCTCTGCCAGGCGCCGCGCCGGGCTCTCTCACTG
CTCCTTCACTCACTACCGTGGTCTGCTGCAATGCTGCTGCAAGCTCGTGTACCTGGCTC
CTCGTGCAGCACTCAGAGGATGAGGACAGCCAAATCGCGTGGCTGTACACCTTTGTCTAC
CCCTTACTCAACCTTTGCTTTACAGCCTTAGGAACAAGGATGTCAAAGGTGCTCTGAGG
AGTGCCATTATCCGTAAGCAGCCTCTGACGCCAACTGA (SEQ ID NO: 190)

45
AOLFR103 sequences:

MAEMNLTLVTEFLLIAFTEYPEWALPLFLLLFMYLITVLGNLEMIIILMDHQLHAPMYFLLSH
LAFMDVCCYSSITVPQMLAVLLEHGAALSYTRCAAQFFLTFPGSIDCYLLALMAYDRYLAVCQ
50 PLLVYTLTQARLSLVAGAYVAGLISALVRTYSAFTLSFCGCTSEIDFPCDLPPLLLKTGCESYT
QVLIUMFAIVPASMVVILVSYLFIHAIMGIPAGSQAKFTSTCSHLTAVSLFFGTLIFMYLRG
NSDQSEKNRVVSVLYTEVIPMLNPLIYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)

ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCCTCCTATTGCATTCAGTGAATATC
55 CTGAATGGGCACTCCCTCTCTCTCTCTGTTATATTATGTATCTCATACCGTATTTGGG
AACTTAGAGATGATTATCTGATCTCATGGATCACCAGCTCCACGCTCCAATGTATTTCTCT
CTGAGTCACCTCGCTTTCATGGACGTCTGCTACTCATCTACTGTCCCCCAGATGCTGG

09986505-062201

5 CAGTGTCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCCTTTCT
GTTCACTCTTTTGGTTCATCGACTGCTACCTCTTGGCCCTCATGGGCTATGACCGCTACT
TGGCTGTGTGCCAGGCCCTGCTTTATGTACCACTCTGACACAGCAGGCCCGCTTGAGTCT
TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCCTTGGTGCGGACAGTCTCAGCCCTTC
10 ACTCTCTCCTTCTGTGGAACCAAGTGAGATTGACTTTATTTCTGTGACCTCCCTCTCTGT
AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAGTGCTGATTATTATGTTTGCCATTTT
GTCATCCCTGCTTCATGGTGGTGATCTTGGTGTCTACCTGTTTATCATCTGGTGCCATCAT
GGGATCCCTGCTGGGAAGCCAGGCCAAGACCTTCTCCACCTGCACCTCCCACTCTGCTGCT
GTGTCACTCTCTTTGGTACCTCATCTTCATGTACTTGAGAGGTAACCTCAGATCAGTCTTC
15 GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGGTCATCCCATGTTGAATCCCTC
ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCATATAGAGCC
AAGTTGTCCTAA (SEQ ID NO: 192)

AOLFR105 sequences:

15 MQQLNHTSVSEFILVGFSAFPHLQLMLFLLMYLFTLLGNLLIMATVWRSERLHMPMYFLFC
ALSITEILYTVAIIPRLADLLSTQRSIAFLACASQMFFSFSGFTHSFLLVVMGYDRYVAICHPL
RYNVLMRLRGCTCRVGCWAGGLVVMGVVTSAIHFHLAFCHGKHEIHFFCHVPPLLKLKACGDD
VLVVAKGVGLVCTAILGCLLILLSYAFIVAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS
20 VIYLEPKGPQSPGEDTLMGITYTVLTPFLSPIHSLRNKELKVAMKKTCTFKLPQNC (SEQ ID
NO: 193)

25 ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTGGCTTCTCTGCCTTCCC
CCACTCCAGCTGTGCTCTCTGCTGTTCTGCTGATGTACCTGTTCACGCTGTGGGCA
ACCTGCTCATCTATGGCCACTGTCTGGAGCGAGCGCAGCTCCACATGCCACTGTACCTCTT
CTGTGTGCTCCCTTCCATCACCGAGATCTCTACACGTGGCCA.TCA.TCCCGCGCATGCTG
GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTCGGCTGTGCCAGTCAGATGTTCTT
CTCTTTCAGCTTCGGCTTCAACCACTCCTTCTGCTCACTGTATGGGCTACGACCGCTACG
TGGCCATCTGCCAACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
GGTGGCTGCTCTCGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTGGCCATTTTC
30 CACCTCGCCTCTGTGGACACAAGGAGATCCACCATTTCTTCCCAACGTGCCACCTGTGT
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGAT
ACGGCCCTGCTGGGCTGTTTCTCCTCATCCTCCTCTCTATGCCTTCATCGTGGCCGCCA
TCTTGAAGATCCCTTCTGCTGAAGGTGCGGAACAAGGCCCTTCTCCACCTGTGCCTCTCACT
35 CACTGTGGTGGTGTGCTACTATGGCTTGGCTCCGTCATTTACCTGAAGCCCAAGGTGCC
CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACTACACGGTCTCACACCTTCTCTCA
GCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTGCCATGAAGAAGACTTGCTT
CACCACACTCTTCCACAGAAGCTGCTGA (SEQ ID NO: 194)

AOLFR106 sequences:

40 METANYTKVTEFVLGTLSQTEPVQLVLFVIFLSFYLFILPGNLIHICTISLDPHLTSPMYFLLANLA
FLDIWYSSITAPEMLIDFFVERKIIISFDGCIQLFLLHFAGASEMFLLTVMAFDLYTAICRPLHYA
TLMNQRLLCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDTQVRIACANTPEELVM
ICSSGLISVVCILLALLMSYAFLLALFKKLSGSGENTNRAMSTCYSHITTVLVMFGPSIYIYARPFM
45 SFSLDKVVSVENTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

50 ATGGAACACTGCAAATTACACCAAGGTGACAGAAATTTGTTCTACTGGCCTATCCAGACTC
CAGAGGTCCAACCTAGTCCTATTTGTTATATTTCTATCCTTCTATTGTTCATCTCACAGGCA
AATATCCTTATCATTTTGACCATCAGTCTAGACCTCATCTGACCTTCTCTATGATTGTTCT
GTTGGCTAATCTGGCCTTCTTGATATTTGGTACTCTCCATTACAGCCCTCGAAATGCTCA
TAGACTTTTGTGGAGGAGGAAGATAATTTCTTTGATGGATGCATTGACAGCTCTTCTT
CTTACACTTTGCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGAATGGCCTTTGACCTTCACA
TGTCTATCTGGCGACCCCTCACTATGCTACCATCATGAATCAACGTCTTCTGCTGATATCC
75 GTGGCTCTCTCGGAGGGGGGGCTTCACTTCACTTCTATCATACAGGTGGCTCTCATTTGTC
GACTTCTTCTGTGGGCCCAATGAAGTTAGACAGTTACTTCTGTGATCATACACAGGTTGT
CCGGATTGCTGTGCCAACCTTCCAGAGGAGTTAGTAGATGATCTGTAGTAGGGTCTG
ATCTCTGTGGTGTGTTTGATGTCTGTGTAATGTCTATGCCTTCTCTGGCCTTGTTCAA

GAAACCTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTTCCACATT
ACCAATTGGTGTCTAATGTTTGGGCCATCCATCTACATTTATGCTCGGCCATTTGACTCGTT
TTCCCTAGATAAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCTTTACGTAATCCCAITTA
TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAAATATA
TTTTGTGTAAAGAGAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

MELWNFTLGSGLFVGLNDSGSPELLCATITILYLLALISNGLLLAITMEARLHMPMYLLLGQ
LSLMDLLFTSVVTPKALADFLRRENTISFGGCALQMFALMTMGGAEULLAFMAYDRYVAICH
PLTYMTLMSSRACWLMVATSWILASALIYTVYTMHYPFCAQEIRHLLCEPHLLKLVACAD
TSRYELMVYVMGVTFLLPSLAAILASYTQILLTVLHMPNSNEGRKKALVTCSSHLTVGMGFYGA
ATFMYVLPSSFHSTRQDNISVFYTVTTPALNPLIYSLRNKEVMRLRRVLGKYMPLPAHSTL
(SEQ ID NO: 197)

ATGGAGCTCTGGAACCTTACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
GTGGGCTCTTGAACCTGTCTGTGCTACAATACAATCCATACTTGTGGCCCTGATCAG
CAATGGCCTACTGCTCTCTGGCTATCACCATGGAAGCCCGGCTCCACATGCCATGTACCTC
CTGCTTGGGCAGCTCTCTCTCATGGACCTCTGTTCACATCTGTGTGCTACTCCCAAGGCCCT
TGGGCACTTTCTGGCAGAGAAAAACACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTC
CTGGCATTGACAAATGGGTGGTGTCTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT
ATGTGGCCATTTTGTATCCTCTGACATACATGACCCCTCATGAGCTCAAGAGCCTGCTGGCT
CATGGTGGCCACGTCTGGATCTGGGATCCCTAAGTGCCCTAATATATACCGTGATATACC
ATGCATATCCTCTCTGCAGGGCCAGGAGATCAGGCATCTCTCTGTGAGATGCCACACT
TGCTGAAGGTGGCCTGTGTGATACCTCCAGATATGAGCTATGGTATATGTGATGGGTGTG
GACCTTCTGATTCCCTCTCTGTGCTATACTGGCCTCTATACACAAATCTCTACTCATC
TGCTCCATATGCCATCAAAATGAGGGGAGGAAGAAAGCCCTTGTACCTGTCTTCCACCT
GACTGTGGTGTGGGATGTCTATGGAGCTGCCACATTCATGTATGTCTTGCCACAGTTCCTTCC
ACAGCCACGACAGAACAGCAACATCATCTGTGTTTCTACACAAATGTGCTACTCCAGCCCTGAA
TCCACTCATCTACAGCCTGAGGAATAAGGAGGTCTATCGGGCCCTTGAGGAGGGTCTCTGGG
AAATACATGCTGCCACGACATCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

MCSFFLCQGTGKQAKISMGEENQTFVSKFIHLGLSQDLQTQILLFILIIYLLTVLGNQLIIILFLD
SRLHLTPMYFFLRNLSFADLCFSTSVQVVLVHFLVKKRTISFYGCMTQIIVFLLVGTCECALLAV
MSYDRYVAVCKPLYSTIMTQRVCLWLSFRSWASGALVSLVDSFTFHLPLYWQGNINHYFCE
PPALLKLASIDTYSYSTEMAIFSMGVVILLAPVSLILGSYWNHSTVIQMQSGEGRKLAFTSCGSHLI
VVVLFYSGSIFTYMRPNSTIKLEDKMISVFYTAVTMPLNPIIYSLRNKDVKGALRKLVGRRK
FSHRQ (SEQ ID NO: 199)

ATGTGTCTCTTTTCTGTGCCAAACAGGTAACAGGCCAAAAATCAATGGGGAAGAGAAA
ACCAAACCTTTGTGTCCAAAGTTTATCTTCTGGGTCTTTCACAGGACTTGCAGACCCGATGAT
CCTGCTATTTATCCTTTTCTCTCATCTTTATCTGCTGACCGTGCTTGAAACACAGCTCATCA
TCATTTCACTCTTCTCGGATTTCTGCCTTCACACTCCCATGTATTTTCTTAGAAATCTCT
CCTTTGACAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTGGTGTCACTTCTTGTA
AAGAGGAACCAACATTTCTTTTATGGGTGTATGACACAGATAAATTTCTTCTCTGTTG
GGTGTACAGAGTGTGCGCTGTCTGGCAGTATGTCTATGACCGGTATGTGGCTGTCTGCAA
GCCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTCAGGTCTCT
GGGCCAGTGGGCACTAGTGTCTTAGTAGATACCAAGCTTTACTTTCCATCTTCCCTACTG
GGGACAGAAATATAATCAATCACTACTTTTGTGAACCTCTGGCCCTCTGAAGCTGTGCTTCC
ATAGACATCTACAGACAGAAATGGCCATCTTTCAATFGGCGTGGAATCTCTCTGGCCC
CTGTCTCCCTGATTCTTGGTCTTATTTGGAATATTAATCCACTGTATCCAGATCGAGCT
GGGGAAGGGGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTTGTGTGCTCTCT
CTATGGGTGAGGAATAATTCACCTACATGCGACCAAACTCCAAGACTACAAAGAACTGGA
TAAATGTATCTGTGTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC
TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAACACTGTTGGGGAAGGTGCTTCTCT
CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR109 sequences:

- MLRNGSIVTEFILVGFQSSSTSTRALLFALFLALYSLTAMNGLIHFTSWTDPKLNSPMYFFLG
HLSLLDVCFITTTIPQMLIHVVVRDHVSVCCMTQMYFVFCVGVAEICLLAFMAYDRYVAICY
5 PLNVYPISQKVVCVRLVGTAWFFGLINGFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
WAIFADAIIVLSPMVLTVTSYVHILATILSKASSSGRKFTSTCASHLTVVIFLYTSAMFYSYMN
PHSTHGPDKDKPFSLLYTIITPMCNPPIYSFRNKEIKEAMVRALGRTRLAQPSV (SEQ ID NO:
201)
- 10 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTCAGCAGAGCTCCA
TCTCCACACGAGCATTGCTCTTTGCCCTCTCTTGGCCCTACACGCCTACCATGCGCCATG
AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
TCTTCCCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCACTACCATCCCCACAGATG
15 TTGATCCACCTCGTGGTCAGGGACACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCACTCCTCTTGGCTTTTCATGGCCTATGACCGT
TATGTTGCTATCTGCTACCCACTTAACTATGTCCCAGTCATAAGCCAGAAGGCTCTGTGCA
GGCTTTGGGGAAGTGCCTGGTCTTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTC
ATCTCGAGAGCCCTTCGCGAGAGACAACACATAGAAAGCTTCTCTGTGAGGGCCCCATA
GTGATTGGCCTCTCTGTGGGGACCCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
20 TCGTGGTAATTTCTCAGCCCCATGGTGCTCACTGTCACTTCTATGTGCACATCTCTGGCCACC
ATCCTCAGCAAGGCTCTCCTCCTCAGGTCGGGGGAAGCACTTCTCTACTTGTGCTCTTCAAC
TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTTACATGAACCCCCACAGCACA
CATGGGCGCTGACAAAGACAACCTTTCTCCCTCCTGTACACCATCATACCCCCATGTGCA
ACCCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGGCACTTG
25 GAAGAACCAGGCTGGCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

- MKIANNVTVFTEFILLQTSQDIQLLVFVLILIFYLILPGNFLIFTIRSDPGLTAPLYLFLGNLAF
DASYSFIVAPRMLVDLSEKKVISYRGCTQLFLLHFLGGGEGLLLVMAFDRYIAICRPLHCST
30 VMNPRACYAMMLALWLGGFVHSIIQVVLIRLPCFGPNQLDNFFCDVRQVQIKLACTDMFVVEL
LMVFNBSGLMTLLCFLGLLASVAVILCHVRRRAASEGKNKAMSTCTRVIIIIMFGPAIFYMC
RALPADKMVSLFHTVFPLMNPMIYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:
203)
- 35 ATGAAGATAGCAAAACAACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
AAGATATTACGCTCTTGGTCTTTGTGCTGATCTTAATTTCTACCTTATCATCCTCCCTGCA
AATTTCTCATATTATTACCATAAAGGTGAGACCTCGGGCTCAGACGCCCTCTATTATT
TCTGGGCTCACTTGGCCTTCTCGATGCATCCTACTCCTCATTTGGGCTCCAGGATGTTGG
TGGACTTCTCTCTGAGAAAAAGGTAATCTCTACAGAGGCTGCATCACTCAGCTCTTTT
40 CTTCGACTCTCTTGGAGGAGGGGAGGGAATCTCCTTGTGTGATGGCCTTTGACCGCTAC
ATGCCATCTGCGCGGCTCTGCACTGTTCACTGTCACTGCAACCTAGAGCCTGCTATGCA
TGATGTTGGCTCTGTGGCTTGGGGGTTTGTCCACTCCATTATCCAGGTGGTGCTCATCTCT
CGCTTGCTCTTTGTGGCCCAAAACAGCTGGACAACCTTCTGTGATGTCGACAGGTGA
TCAAGCTGGCTTGACCCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
45 GATGACACTCTGTGCTTTCTGGGGCTTCTGGCTTCCATGCACTCATCCTCTGCCATGTC
GTAGGGGACCTTGTGAAGGGAAGAACAGGCCATGTCCACGTCGACCACTCGTGTGATTA
TTACTCTTATGTTGGACTGCTATCTCATCTCATGTCCTTCTCAGGCGCTTACCA
GCTGACAGATGGTTTCTCTCTTTCACACAGTGATCTTTCCATTGATGAATCTCATGATTTA
TACCTTCCGAACCAAGGAAGTGAACCTTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
50 TGTCAGTGGAATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

- MCYTYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCIHLSILFLLIYLCALM
GNVLIIMITLDDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSLIHNISISFGVSVQFLLSS
55 ASAEILLTVMSFDRYTAICHPLHYDVIMDRSTCVQRTATVSWLYGGLIYMHGTAQTSYSGY
SNMVHQFCDIPQLLAISCSENLREIALILINVLDFCCFVIIITTVHVFSTVKKIPSTEGQSKAY

SICLPHLLVVLFLSTGFIAYLKPASESPSILDAVISVFYTMLPPTFNPIHYSLRNKAIKVALGMLIKG
KLTKK (SEQ ID NO: 205)

5 ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
TTTCTCGCAGATTACTCTGCAATAATGGCAAATCTCACAATCGTGAAGTAAATATCCTTA
TGGGGTTTCTACCAATAAAAAATATGTGCATTTTGCAATCGATTCTCTTCTGTGATTAT
TTGTGTGCCCTGATGGGGAATGTCCTCATATCATGATCAACAATCTTGGACCATCATCC
ACACCCCCGTGATATTTCTCTTGAAGAATCTATCTTTCTGGATCTCTGCGCTATTTCAGTC
10 ACGGCTCCCAATCTATCGCAAATCTTTTGATACACAACAACCTCCATTTCATTCTTGGCTG
TGTITCCGAGGCTTTTGTGTGCTTCTTCAGCATCTGCAGAGCTGCTCCTCCTCAGCGTGA
TGTCCTTTGACCGCTATAGCTATATGTACCCCTCTGCAATGATGTCAATCATGGACAGG
AGCACCTGTGTCCAAAGAGCCATGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC
ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAAACATGGTCCATCAGTCTTCTGT
GACATTCGCCAGTATTAGCTATTTCTTGCTCAGAAAAATTAATAAGAGAAAAATGCACTCA
15 TCTTATTAATGTAGTTTGTGATTTCTGCTGTTTATTGTGCATCATCTAACCTATGTCAC
GTCTTCTCTACAGTCAAGAAGATCCCTCCACAGAAGGCCAGTCAAAGCCACTCTATTT
GCCTTCCACAGTGTGCTGGTGTGTGTTATTTCTTCCACTGGATTCAATGCTTATCTGAAGCCA
GCTTCAGAGTCTCCTTCTAATTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCC
AACCTTTAATCCCATATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
20 TTGATAAAGGGAAGCTCACCAAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

MKFVHGFSSHLNPMFSSFLLYSLPWINTTQAWNLCLSLALPVWAMSGAGFLSCCYWHTCSP
SVVTCSSSSQSSDWMQLCTHLCTTLVFFPWSWCGIQLPLSLRCLLFSVRRKPFLLQDASFRPTSS
25 TPWGACEFCYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF
CAYNEQHIFCDPPLLSLACKDTSANILVDFAINAFILITFFIMISYARIGAVLKKIKTASGRKK
AFSTCASHLAVVLIFFGSIFMYVRLKKSYSLLDRTLTAIVYSVLTMPMVNPIHYSLRNKEIKAIKR
TIFQKGDKASLAHL (SEQ ID NO: 207)

30 ATGTGTCAACAAATCTACGGGATTGCATTCTTCTCATACATCATTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGTCTATAACCCACACAATGGAAACCCCTGCCTC
CTTCTCCTTGTGGGTATCCCAAGGACTGCAATCTTCACTCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
35 TTCCATCTCGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTA
TGCCCTCCTCGGTGGTACCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGTCTGTTTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTTCTCAGCCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTACAT
AGCCATAACTCCACTGAGTGTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
40 GTCCATCTCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCA
GCACTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCTCTTCAATGTCT
GCCTCTATCTTAATTTCTCAAGGCAGTATTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGATCTATCTACTCTGGGATTG
45 GCATCCATCTATGCGCGCTGGTTGGGGCAGGATGTAGTGCCTTGCACCAACCAAGTCTGC
TAGCTGACCTGTACGTGATCATCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAG
CAACAACTGCGGGAGAGAAATGGAAGTATCTGATGCATGTCTCTTGTACCATTCCAAC
CTGGGTTCATGA (SEQ ID NO: 208)

AOLFR114 sequences:

50 MERINHTSSVSEFILLGLSSRPEDQKTLFVLFLIVLYVTITGNLLIILAIRFNHQLTPMPYFFLSFLS
LTDICFTTSVVPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSLAVMAFDTRYVAVCDPF
HYVTMSHHCVLLVAFSCSPHLHLLHTLLNRLTFCDNVHHFLCDLSPVLKLCSSSIFVN
EIVQMTAPIVLTVRFLCIAFSYIRILTVLTKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLOP
PSTYAVKDHVATIVYTVLSSMLNPFHYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

55

5 TTGCCAGTTGGTTCTGGCATGGCTTGGAAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
TATATTTTGATTCGTACTCTGTACTTAGACTGAACCTCAGCTGAAGCTGCAGCCAAAGGCC
TGAGCACTTGTAGTTACACATCTCACCCCTACCTTTCTTTACACATTTGTTGTAGTGATT
TCAGTGACTCATCTGCAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTGC
ACAACATCATCCCCCTTCCCTCAACCTACAGTTTATGCACCTTCAGACCAAGAACTTAG
GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

AOLFR119 sequences:

10 MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIHIFVGNLGLVYLIYYEESLHHP
MYFFFGHALSLIDLTTCTTLPNALCIFWFSLEKINFNACLAQMFFVHGFTGVESGVLMMLALD
RYIAICYPLRYATTLNPNIAKELATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL
SCASIKVNVIVGLMVALLIGVFDICCSLSYTLILKAAISLSSDARQKAFSTCTAHISAIHITYVPA
15 FTFFAHRFGGHTIPPSLHIVANLYLLPPTLNPVIVGVKTKQIRKSVIKFFQGDKGAG (SEQ ID
NO: 219)

20 ATGCCCTCTATTTAATTCAATTAGCTGGTTTCCAAACAATTCACTGTGACTCTCCATCTTTTAT
TCTTAATGGAATCACTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCCTCTGCACA
ATGTACATCATCTTCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC
CTTACATCATCCGATGTATTTTCTTGGCCATGCTCTCTCCCTCATTAAGACCTCTTACCTG
CACCACCACTTACCCTCAATGCACTCTGCATCTCTGGTTCAGTCTCAAAGAAATTAACCTTCA
ATGCTTGCTTGGCCAGATGTTCTTGTTCATGGGTTACAGGTTGGAGTCTGGGGTGCT
CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCCTTGGCTTATGCTACCCAC
TCACCAACCTATCATTGCCAAGGCTGAGCTTGCCACCTTCTGAGGGGTGTATTGCTGAT
25 GATTCCTTTCCCATTTCTGGTTAAGCGTTTGCCCTTCTGCCAAAGCAATATTATCTCCCA
CGTACTCGGACCACATGCTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCATGTAAT
CTATGGTCTAATGGTGTCTCTGATGGAGTGTITGACATTTGTGTATATCTTGTGCTT
ACACTTGTATCTCAAGGACGCGATCAGCTCTCTCATCAGATGCTCGGAGAAAGCTT
30 CAGCACCTGCACTGCCATATATCTGCCATCATATCACTATGTTCCAGCATTTCTTCACCTT
TCTTTGCCCAACCGTTTGGGGGACACAAATCCCCCTCTCTTCACATCATTTGTGCTAAT
CTTTATCTTCTCTCCCCCACTTAAACCCCTATTGTTATGGAGTAAAGACAAAACAGAT
ACGCAAGAGTGTCAAAAGTTCTTCCAGGGTGATAAGGGTGACAGTTGA (SEQ ID NO: 220)

AOLFR120 sequences:

35 MQPYTKNWQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENAILLVGLDHLRRPMPYF
FLTHLSLEIYWYTVTPKMLAGFIGVDGGKNISYAGCLSQLFIFFLGATECFLLAAMAYDRY
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPILPYLLSQLTFCGPNVIDHFSDDASPLLARS
CSDVWTKETVDFLVSLAVLLASSMVIASVYGNIVWTLHLIRSAERWKAFTSCAAHLTVVSLF
40 YGTLFFMYVQTKVTSINFNKVVSVFYSVTPMLNPLIYSLRNKEVKGALGRVFSLNFWKQG
(SEQ ID NO: 221)

45 ATGCAACCATATACCAAAAACCTGGACCCAGGTAACCTGAATTTGTATGATGGGCTTTGCTG
GCATCCATGAAGCACACCTCTCTCTTCATACCTCTCCCTCACCATGTACCTGTTCACCTGT
GTGGAGAATTTGGCCATCATTTTGTGTTGGGTTTGGACCACCGACTACGGAGACCCATGT
ATTTCTCTGCACACACTTGTCTGCTTGGAAATCTGGTACACTCTGTTACAGATGCCAAG
ATGCTGGCTGGTTTATTTGGGTTGGATGGTGGCAAGAATATCTCTATGCTGGTTGCTAT
CCCAGCTCTTCATCTTCAACCTTCTTGGGGCAACTGAGTGTTCCTACTGGCTGCCATGGCC
TATGATCGTTATATGGCCATTTGTATGCCTCTCCACTATGGGGCTTTGTGTCTGGGGCAC
50 CTGCATCCGCTCGGCAGCTGCCTGTTGGCTGGTAGGTTCTCTCACACCCATCTTGCAACTCT
ACCTCTGTGCTCAGCTAACATTTTGTGGCCCAATGTCATGACCATTTCTCTGTGATGCC
TCACCCCTGTGAGCCTTGTGCTGCTCAGATGTCACTTGAAGGAGACTGTGGATTTCCTGG
TGTCTCGGCTGTGCTACTGGCTCTCTATGGTCAATTGCTGTGTCCTATGGCAACCTGCT
TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCTCTCTCACTGCTGACG
60 CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTCTTATGATGTGCCAGACCAAG
GTGACCTCTCCATCAACTCAACAAGGTGGTATCTGTCTTCTACTCTGTGTACGCCCCAT

0000055-06201

GCTCAATCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTCGAGTC
TTTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

AOLFR121 sequences:

5 MKRKNFTEVSEFIFLGSSFGKHQITLFVVFLTVYILTLVANIIIVTIICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPSLAGCATQMFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAAMFNLPFCGTVDHFFCDIYPMKLSCIDTTINEII
NYGVSSFVPIGLIFISYVLVISSILQIASAEGRKKTATCVSHLTVVIVHCGCASLAYLKPSES
SIEKDLVLSVITYIITPLNPNVVSILRNKEVKDALCRVVRNIS (SEQ ID NO: 223)

10 ATGAAGAGAAAAGAACTTCACAGAAGTGCAGAAITCATTTTCTGGGATTTTCTAGCTTGT
GAAAGCATCAGATAACCCCTCTTTGTGGTTTCTCTAACTGTCTACATTTAACTCTGGTGTCT
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTCTCT
CCTAAGCATGTGGCTAGTTCAGAGACGGGTGACACACTGGTTCATTGTGCCACGAATGCTT
15 TTGAGCCTCATTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGTACACAAATGTCTT
TTTGTATCTTGGCCACTAATAATGTCTTCTGCTTACTGCAATGGGGTATGACCGCTATG
TGGCATCTGCAGACCCCTGAGATACACTGTATCATGAGCAAGGGAATGTGCGCCAGCT
GGTGTGTGGGTCTTTGGCACTTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTT
AATTGTGGCTTCTGTGGCACAGTGGTAGACCCTTCTTTGTGACATTTAGCCAGTCATGA
20 AACTTCTGTGCATTGATACCACTATCAATGAGATAATAAATATGTGTGAAGTTCATTGTG
GATTTTGTGGCCATAGGCCTGATATTTATCTCCTATGTCTTGTATCTCTTCCATCCTTC
AAATGTGCCTGAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCAGTGT
GGTTATTGTGCACTCTGGCTGTGCCTCATTGCTACCTCAAGCCGAAGTCAAGCAAGTTCA
ATGAAAAAGACCTTGTCTCTCAGTGACGTACACCATCATCACTCCCTTGTGAACCTGT
25 TTGTTTACAGTCTGAGAAACAAGGAGGTAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

30 MEWENQTLVEFFLKGHSVHPRLELLFFVLIFIMYVILLNGTLILISILDPHLHTPMYFFLGNL
YPLDICYTTISIPSTLVSLFSEKTSFSGCAVQMFGLAMGTCEVLLGMMAFDRYVAICNPLR
YPIIMSKYVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCILAVMKLACASIGN
EFLMLVATILFTLMPLLLIVISYSLIISILKHSSEGRSKAFSTCSAHLTVVIFYGTILFMYMKPKS
KETLNSDDL DATDKIISMFGVMTMPMNPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:
225)

35 ATGGAATGGGAAAACCAACCATCTGGTGAATTTTCTGAAGGGACATTCTGTTCACC
CAAGGCTTGAGTACTCTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTAAATCAGCATCTTGAGCCCTCACCTTCACACCCCATGTACTTCTT
TCTGGGGAACCTCTCCTTGGACATCTGCTACACCAACCACTCTATTCTCCCTCCACACTAG
40 TGAGCTCTCTTCAGAAAGAAAGACCATTTCTTTTCTGGCTGTGCAAGTGCAGATGTTCCTT
GGCTTGGCCATGGGACAACAGAGTGTGTGCTTCTGGGCAATGATGGCCTTGTAGCGCTATG
TGGCTATCTGCAACCTCTGAGATATCCCATCATCATGAGCAAGAAATGCCTATGTACCCAT
GGCTGTGGGTCTGGTTTGACGGGATTGTCACTCTGCAGTACAACATCATTTGTAGTA
CAATGTGCCTTCTGCAGGAAGAAATGTATCAATCATTTCTCATGTGAAATCTAGCTGTGAT
45 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCCTCATGCTTGTGGCCACAATATTG
TTCACATGATGTCACATGCTCTTGATAGTATCTTACTCATTAATCATTTCCAGCATCT
CAAGATTCACTCCTCTGAGGGGAGAAAGCAAAAGCTTTCTCTACCTGCTCAGCCATCTGACT
GTGGTCAATAATTCTATGGGACCATCTCTTCTCATGTAATGAAAGCCCAAGTCTAAAGAGA
CACTTAATTCAGATGACTTGGATGCTACCGACAAAATATATCATGTTCTATGGGGTGAT
50 GACTCCCATGATGAATCTTTAATCTACAGTCTTGAACCAAGGATGTGAAGAGGCAGT
AAAACACCTACCGAACAGAAGGTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

55 MYRFTDFDVSNISYLVNHLVFTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPEQLFLFLCL
IMYMIILLGNSLLIITLIDSLRHTPMYFFLGNLSFLDICYTSSSIPMLLIIFMSERKSISFIGCALQM
VVSILGNGTCEVLLAVMAYDHYVAICNPLRYSIIMNGVLVYQMAAWSWIIGLTSLLQTVLT

MMLPFCGNNVIDHITCEILALLKLVCSDI[TINVLMITV]TNVSLVILLLLIFISYVFLSSILRINCAE
GRKKAFSTCSAHSIVILFYGSALFMYMKPKSKNTNTSDEIGLSYGVVSPMLNPIIYSLRKEV
KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

- 5 ATGTACAGATTTACAGATTTTGTATGTATCAAAACATTTCAATTTACCTGAATCATGTCTTTT
CTATACTACCCAGCAGGCGAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
GACTGAATTTCTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTCTGTCTCTGC
TCTGGCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCAATTATCATCAACATC
TGTGATTTCTCGCTCCATCTCCCATGTATTTCTTTCTTGGAAACCTCTCATTTCTTGACAT
10 CTGTTACACATCCTCATCCATTCTCCAATGCTTATTATATTTATGTCTGAGAGAAAAATCCA
TCTCCTTCATTGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT
GTCTCTCTGGCTGTGATGGCCTATGACCCTATGTGGCCATCTGCAACCCACTGAGGTACT
CCATCATCATGAACGGAGTGCTGTATGTGCAAATGGCTGCATGGTCTGGATCATAGGCTG
TCTGACCTCCCATTTGCAACACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC
15 ATTGATCATATTACCTGTGAAATTTGGCCCTTCTAAAACCTGTTTGTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTTCTTCACTGTTAATT
TCATCTCTATTGTGTTATTCTCTCTTCCATCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTCAAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
TTTTATGTACATGAAACCCAAGTCAAAGAACCTAATACATCTGATGAGATTATTGGGCTG
20 TCTTATGGATGGTGAAGCCCAATGTTAAATCCCATCTATAGCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ
ID NO: 228)

AOLFR124 sequences:

- 25 MNHSVUTEFIILGLTKPELQGIIFLFLVYLVAFLGNMLIIIAKIYNNLTHTPMYVFLTLAVV
DICTTSHIPKMLGTMLTSENTISYAGCMSQLFLTWSLGAEMVLFTTMAYDRYVAICFPLHYST
VMNHMMCVALLSMVMAIAVNTSWVHTALIMRLTPCGPNTIDHFFCEIPLALLSCSPVRINEV
MVVYADTLAGDFILTCISYGIIVAILRIRTVGKRKAFTCSSHLVTVLYYSPKDIYTYIRPASS
YTFERDKVVAALYTLVTPTLNPMVYSFQNRMQAGIRKVF AFLKH (SEQ ID NO: 229)
- 30 ATGAATCACAGCGTTGTAACCTGAGTTCATTATTCTGGGCCCTCACAAAAAGCCTGAACCTCC
AGGGAATTATCTCTCTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
ATCATCATTTGCCAAAATCTATAACAACACCTTGCATACGCCCCATGTATGTTTCTCTTGAC
ACTGGCTGTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
35 GCTAACCATGAAAATACCAATTTATATGCAAGCTGCATGCCCCAGCTCTTCTTGTTTACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCATGACCCGCTATGTGGCCA
TTTGTTTCCCTCTTCATACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
ATGGTCATGGCTATTGCACTACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
CTTTCTGTGGGCCAAACACCATTGACCACTCTTCTGTGAGATACCCCATTTGCTGGCTTGT
40 TCCCTGATGCCCTGTGAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCTGGCCA
TAGGGGACTTTATTCTACCTGCATCTCCTATGGTTTTATCATTTGTTGCTATTCTCCGTTG
CGCACATAGAAAGGCAAGAGGAAGGCCCTTCAACATGCTCATCTCATCTCAGCTGATG
ACCTTTTACTATTCTCTGTAATCTACACCTATATCCGCCTGCTTCCAGCTATACATTGA
AAGAGACAAGGTGGTAGCTGCATCTATACTCTTGTGACTCCACATTAAACCCGATGGTG
45 TACAGCTTCCAGAATTAGGAGATGACGGCAGGAATTAGGAAGGTGTTGCAATTCTGAAA
CACTAG (SEQ ID NO: 230)

AOLFR125 sequences:

- 50 MTNQTQMMFLLVRFTENWVLLRLHALLFSLYLTAVLMNLVILLMILDHRLHMAHYFFLRH
LSFLDLCLISATVPKSLNSVASTDSISLFCVLQLFLVLLAGSEIGILTAMSYDRYAACCPHLH
EAVMSRGLCVQLMALSWLNRGALLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSEKHA
ISVSAIGVCYAFSCLVCIIVSYVYFSAVLRISQRQRQSAFNSNCPHILVTVFLVTGAVAYL
KPGSDAPSIILLVSVFYVAPPTLNPVYICLNKNDIKSALKSVLWNVNRSSGMPDII (SEQ ID
NO: 231)

55

ATGACCAATCAGACACAGATGATGGAATCTTGTCTGTGAGATTTACTGAGAATTTGGGTGC
 TCTTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCAGGCTGTGCTGATGAATTTA
 GTCATTCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCG
 5 ACATTITGCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCCAAAATCCATCTCAACT
 CTGTGCGCTCCACTGACATCCATCTCCTTCTGGGGTGTGTGTGACGCTCTCTTGGTGGTA
 CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCTATGACCGCTATGCTGCCA
 TCTGCTGCCCTACACTGTGAGGCTGTCAAGCAGAGGGCTCTGTGTCCAGTTGATGGC
 TCTGTCTGGCTCAACAGAGGGGCTTGGGACTCTTGTACACAGCTGGAACATCTCTCTG
 AATTTTTATGGCTCTGATGAGCTACATCAGTCTTCTGCGATGTCCCTGCCCTACTAAAGT
 10 CACTTGTCTAAAGAACATGCCATCAITAGTGTCACTGTGGCCATTGGGGTCTGTATGCA
 TTTTCATGTTTGTGATTGTAGTTTCTCATGTGTACATTTTCTGCTGTGTAAAGAT
 ATCAGAGACAGAGAGAACATCCAAAGCCTTTCCAACTGTGTCCCTCACTCACTGTGTGTC
 ACTGTGTTTCTGTAAACAGGTGCTGTGTCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
 TCTAGACTTGTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTGAACCTGTTATCT
 15 ACTGTCTGAAGAACAGGACATTAATCCGCTCTGAGTAAAGTCTGTGGAATGTTAGAA
 GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

MFYLLCFIFQRTCEEMEEENATLLTEFVLTFGLHQDPCKIPLFLAFLVIYLITIMGNLGLIVLIW
 20 KDPHLHIPMYLFLGSLAFVDASLSTVTPKMLINFLAKSMISLSECMVQFFSLVTTVTTECFLL
 ATMAYDRYVAICKALLYPVIMTNELCIQLVLVSLFGILLHALIHEAFSRLTFCNSNIIHFYCDII
 PLLKISCTDSSINFLMVFIAGSVQVFTIGTILISYTHLFTILEKKSIGKIRKAVSTCGAHLISVSLY
 YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
 NO: 233)

ATGTTCTCTTACCTTTGCTTCATTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
 ATGCAACATTTGCTGACAGAGTGTGTTCTCACAGGATTTTACATCAACCTGACTGTAATAA
 ACCGCTCTTCTGGCATCTTGGTAATATATCTCATACCATGCTGGGGAATCTTGGTCTAA
 30 TTGTTCTCATCTGGAAGAACCCCTCACCTTCATATCCCAATGTACTATTCTCTGGGAGTTTA
 GCCCTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTCTTAG
 CTAAGAGTAAGATGATATCTCTCTGAAATGCAATGTAACAATTTTTCCTCTGTAACCACT
 GTAACCAAGCAATGTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTTGCA
 AAGCTTTACTTTATCCAGTCATTATGACCAATGAACATGCACTTCACTGATGCTTGTGCA
 TTTATAGGCTGGCCCTCTTCATGCTTTAATCCATGAAGCTTTTTCATGACATTAACTTCTG
 35 TAATTCGAACATAATACAACACTTTTACTGTGACATTTATCCCATTTGTTAAAGATTTCTGTA
 CTGATTCCTCTAATTAATTTCTAATGGTTTTATTTTCGCAAGTTCTGTTCAGTTTATTACCA
 TTGGAAATCTTCTAATATCTTATACAATATCCTCTTTACAATCTTAGAAAGAAAGTCTATC
 AAAGGGATACGAAAGCTGTCTCCACCTGTGGGGCTCATCTCTATCTGTATCTTTATACT
 40 AACTGCCCTTCACTTCAATATCTGGGCTGTGCATCTCCGAAGCAGATGAACCAAGATAT
 GATGGAGTCTCTATTTTACACTGTCTATGTTCTTTATTAATCCCATGATCTACAGCTGA
 GAACCAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAGCAATGTTTAG (SEQ ID
 NO: 234)

AOLFR127 sequences:

MSNEDMEQDNTLLTTEFVLGTLYQPEWKMPFLVFLVIYLITIVNWLGLIALIWNPDQLHIPM
 45 YFELGSLAFVDAWISSVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
 VAICKPLLYPVMNNSLCIRLLAFSLGGFLHALIHEVLIFRLTFCNSNIIHFYCDIPLFMISCTD
 PSINFLMVILSGSQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLISVSLYVGPLIF
 MYLRPASPPQADDQDMDSVFYTHIPLNPIHYSRLNKKQVIDSFTKMYKRVN (SEQ ID NO: 235)

ATGTGCAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTCTCACA
 GGACTTACATATCAGCCAGAGTGGAAAAATGCCCTCTTCTTGGTGTCTTGGTGATCTATC
 TCACTACTATTGTGGAACTTGGTCTGATGTCTTATCTGGAATGACCCACAACCTTAC
 55 ATCCCATGTACTTTTCTTGGGAGTTAGCCTTGTGTGATGCTGGATATCTTCCACAGT
 AACTCCCAAAATGTGTGTAATTTCTTGGCCAAAAACAGATGATATCTCTGTCTGAATGC
 ATGATTCAAATTTTTCTTGTGCTTGGTGGAACTACAGAATGTTTCTCTGGCAACAAT

GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTATATCCAGTGATTATGAACAAT
 TCACATTCGATACGGCTGTAGCCCTTCATTTTTAGGTGGCTTCCTCCATGCCTTAATTCAT
 TGAAGTCCTTATATTTCAGATTAACTCTCTGCAATTCTAACATAATACATCATTTTTACTGTG
 ATATTATACCACTGTTTATGATTTCCTGTACTGACCCCTCTATTAAATTTCTAATGGTTTTTA
 5 TTTTGTCTGGCTCAATTACGGTATTCACCATTTGTGACAGTTCTTAATTTCTACACATTTGCT
 CTTTTCACAACTCTAAAAAAGAGTCTGTAGAGGCGTAAGGAAAGCCCTTTTCCACCTGTG
 GAGCCCATCTCTTATCTGTCTCTTATATTATGGCCCACTTATCTCTATGTTTGTGCGCCCT
 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTATACATATCATAATTC
 10 CTTTGGCTAAATCCCATATCTACAGTCTGAGAAATAACAAAGTAATAGATTCAATTCACAAA
 AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

METQNLTVVTEFILLGLTQSDAQLLVFLVLFIYLIILPGNFLIIFTIKSDPGLTAPLYFFLGNLA
 LLDASYSFIVVPRMLVDLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMAFDRYIAICRPLHY
 15 STIMNPRACYALSLVLWLGGFHSIVQVALILHLPFCGNQLDNFFCDVPQVIKLACTNTFVVVEL
 LMSVNSGLSLLCFLGLLASYAVILCRIEHSSEKSKAISTCTTHIIIFLMFGPAIFIYTCPQAF
 ADKVVSFLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMF (SEQ ID NO: 237)

ATGGAACACAGAACCCTCACAGTGGTGACAGAATTCATTCTTCTGGTCTGACCCAGTCTC
 AAGATGCTCAACTCTGGTCTTTGTGCTAGTCTTAATTTCTACCTTATCATCTCCCTGGTA
 20 AATTTCTCATCATTTTACCATAAAGTCAGACCTGGGCTCAGACCCCTCTAATTTCTT
 TCTGGGCAACTTGGCCTTACTGGATGCATCTTACTCTTCATTGTGGTTCGGAGATGTTG
 GTGGACTTCTCTCTGAGAGAAGAAGTAATCTCTATAGAAGCTGCATCACTACGCTCTTTT
 TCTTGCATTTTCTGGAGCGGGAGAGATGTTCTCTCGTTGTGATGGCCTTTGACCCGCTAC
 25 ATCGCCATCTGCCGCGCTTTACACTATTCAACCATCATGAACCCCTAGAGCCCTGTATGAT
 TATCGTTGGTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
 CACTTGCCTTTCTGTGGCCCAACACAGCTCGATAACTTCTCTGTGATGTTCCACAGGTCAT
 CAAGCTGGGCTCGACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCAACAGTGGCCTG
 CTGAGCTCTCTGTGCTTCTGGGCTTCTGGGCTCCTATGCAGTCACTCTCTGTGATTAAG
 30 GGAGCACTCTCTGGAAGGAAGAAGCAAGGCTATTCCACATGCACCAACCATATATTCAIT
 ATATTGCTCATGTTTGGCACTGCTATTTTCACTACACTTGCCCTTCCAGGCTTCCCAAGC
 TGACAAGCTAGTTTCTTTTCCATACTGTCACTTCTCTGTGATGAACCCCTGTTATTTATA
 CGCTTCGAACCAAGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTGG
 35 CTGA (SEQ ID NO: 238)

AOLFR129 sequences:

MALYFSLILHMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLTSSQDVEFLFALFSVI
 YVTVLGNLLIIVTVFNTPNLTNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
 40 QIFLLHLLGGVEMVLLVSMFAFDRYVAICKPLHYMTIMNKVVCVLLVVTSWLLGLLHSGFQIFP
 AVNLPFCGNPVDSIFCDLPLVTKLACIDIYFVQVIVVANSGHLSFCFILLISYSLIITIKNHSPT
 GQSKARSLTAHTIVVILFFGPCIYIWPFGNHSVDKFLAVFYTIITPILNPIYTLRNKEMKISM
 KLWRFAVNSREDT (SEQ ID NO: 239)

ATGGCTCTTTATTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTCTCTACAGG
 45 TCATCCAAAGAGCGAGCTGTAGGATGGAGCCATGAAACTATTAACTCAATCTCAAGTGTG
 AGAATTCATTTTGTCTGGGACTGACCAGCTCCAGGATGTAGAGTTTCTTCTTGGCCCTCT
 TCTCGGTATCTATGTGGTCACAGTTTGGGTAACCTCTTAATTATAGTCACAGTGTTTAAC
 ACCCTTAACCTGAATACCTCCATGTATTTTCTCTTGGTAATCTCTCTTTGTAGATATGAC
 CTTTGTCTCTTTTGGCAACCCTAAGGTGATTCTGAACTTGTAAAAAAGCAGAGGTAATT
 50 CTTTGTCTGGGTGCTCACTCAGATATTTCTCTTCACTTACTGGGTGGGGTTGAAATGGT
 ACTGTTGGTCTCCATGGCTTTGACAGATATGTGGCCATTGTGAAGCCCTACACTACATG
 ACCATCATGAACAAGAAGGTATGTGTTTGTCTGTAGTGAACCTATGGCTTCTGGGTCTCC
 TTCACAGGGTTTCAGATAACCATTTGCTGTGAACCTTGCCCTTTTGTGGTCCCAATGTGGTA
 55 ACAGGTATCTTTTGTGACCTCCCTTTGGTTACTAAGCTTGAGCTGTATAGACATATATTTGT
 TCTCTACAGCTGATCTCATAACCATTAAGAACCCTCTCTACTGGGCAATCTAAAGC

CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTTGGCCCATGCATCTTTA
TCTACATTTGGCCCTCGGCCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTATACCACT
ATCACTCTCATCTTTGAATCCAATTATCTATACTCTGAGAAAAAGAAATGAAGATATCCA
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

5

AOLFR131 sequences:

MASTSNVTELIPTGLFQDPQAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
LVEISYSSSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFFGVAEILIVMAYDVCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSHIQLVIIQLPFCGPNVIDHYFCDLQPLFKLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYVIVLVLNRHNSABGRHKALSTCASHITVILPFGPAIFLYMRPSSTFTED
KLVAVFYTVITPMLNPIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

10

ATGGCCAGTACAAGTAATGTGACTGAGTGTGATTTTCACTGGCCTTTCCAGGATCCAGCTG
TGCAGAGTGTATGCTTTGTGGTGTTTCTCCCGGTGACCTTGCCACGGTGGTGGGCAATGG
CCTCATCTGTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTCTTCTCTTA
TGCGCTGTCTCTGGTGGAGATCAGTTAATCTCCACTATCGCCCTAAATTCATCATAGAC
TTACTTGGCAAGATTAACCACTCTCTGGAAGGCTGTCTGACTCAGATATTCTCTTCCCA
CTTCTTTGGGGTGTCTGAGATCCTTTGATTGTGGTGATGGCTATGATGCTACGTGGACCT
ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTCACTCTCTGGTGGC
TGGTCTCTGGCTGGGGGGCTTTGTCACTCCATAATTAGATTCTCGTTATCATCCAATGTC
CCTCTGTGGTCCCAATGTGAITGACCACTATTCTGTGACCTCCAGCCTTATTCGAAGCTT
GCCTGCATGCAGCACTTCAATGGAGGGGGTTATGTGTGTGGCAACAGTGGATTATCTCTG
TCTCTCCCTTCTCATCTCTGGTGCTCTTATATGTGCTATTCTGGTCAACTTGAGGGAACCAT
TCTGCAGAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTACATCAGAGTGCATCT
25 TGTTTTGTGACCTGTATTCTTCTCTACATGCGACCTTCTCCACTTTCACTGAAGATAAA
CTTGTGGCTGTATTCTACACGGTCACTACCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

20

25

AOLFR132 sequences:

MVATNNVTIEIFVFGSQNWSEQRVISVMFLMYTAVVLGNGLIVLTVLASKVLTSMPYFFLSYL
SFVEICYCSVMAPKLFDSFIKRKVISLKGCLTQMFLHFFGGTEAFLMMVAYDRYVAICKPL
HYMAIMNQRMCGLLVRIAWGGGLHSHVQTLIFLQPCGPNIMDHYFCDVHPVLEACADT
FFISLLIITNGGISVSVSFFVLMASYLILHFLRSHNLEGQHKALSTCASHVTVVDFPFCSLVYIR
35 PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIFGGKVI (SEQ ID NO: 243)

30

40

45

50

ATGGTGTGTCACAAACATGTGACTGAAATAATTTTCGTGGGATTTTCCAGAAATGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCTCATGTACACAGCTGTGTGGCTGGGCAATGG
CCTCATTTGGTGACCATCTCGGCCAGCAAGTGCTCACTCCCCATGTATTCTTCTTCA
GCTACTTATCCTTTGGAGATCTGCTACTGTTGTGTCATGGCCCCAAGCTTATCTTGAC
TCTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTCTCCCTC
ATTTCTTTGGTGGCAGCTGAGGCCCTTCTCTGATGGTGATGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACAGCGAATGTGTGCTCTCTCGTG
AGGATAGCATGGGGCGGGGGCTGTGCTGCTGTTGGGCAACCTTCTGATTTTCCAGC
TCCGCTCTGTGGCCCCAACATCATGACCACTACTTCTGTGATGTCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTCATTAGCCTGCTGATCATCAACCAATGGCGGCTCCATC
TCCGTAGTCAGTTTCTTCTGCTGATGGCTTCTCACTGATCATCTGCATCTTCTGAGAAG
CCACAACCTGGAGGGGCGACACAAGGCCCTCTCCACTGTGCTCTCATGTCAAGTTGTC
GACCTGTTCTTACACTTGTCTCTTGGTCTATATTAGGCCCTGTGACCCCTCCCTGCAGA
CAAGATAGTTGCTGTATTATTTATACAGTGGTCACACCTCTCTTAAACCTTGATTTACTCTC
TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTTATTGGGGGAAAAAGTAATTTGA
(SEQ ID NO: 244)

AOLFR133 sequences:

MTEFIFLVLPNQEVQRVCFVIFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWGCMAQLFHLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN

55

0986055_062201

WQVCTVLVGIAWVGGFMHSFAQILLIFHLLFCGPNVINHYFCDLVLPLKLACSDTFLIGLLIVAN
GGTLSVISFGVLLASVMVILLHLRITWSSEGWCKALSTCGSHFAVVILFFGCPVFNLSRPTTLPI
DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

- 5 ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTGTACACAGCAATTGTGCTGGGGAATTCTCTATTGTGCTCACTGTC
ATGACACAGAGAAGCCTTGGTTCCTCCCATGTACTTCTCCTCAGCTACCTCTCTCATGGA
GATCTGCTACTCTCGCTACAGCCCCCAAACTCATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTCTTGCACTTCTTTGGTGGCACTGA
10 GATTTTCTGCTCACTGTGATGGGCTATGACCACTATGTGGCACTCTGCAAGCCCTCAGC
TACCCACCATCATGAACCTGGCAGGTGTGTACTGCTCTGTAGGAAATAGCATGGGTGGGA
GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTCTGTGGCCCAA
TGTGATCAATCACTATTTCTGTGACCTAGTTCCTCTCTCAAACCTGGCTGCTCTGACACT
TCTCATTTGGTCTGCTGATTTGTGCCAAATGGAGGCACCCCTGTCTGTGATCAGTTTGGGGT
15 CCTCTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
TGCCAAAGCCCTCTCCACCTGTGGGTCCCATTTGCTGTGGTTATCTGTCTTTGGGCCCTG
CGTCTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGCTGTGTTCT
ACACAGTGATAACCGGATCTGCAACCCTGTCTACTCTCTGAGAAATGCTGAAATGAG
GAAGGCCATGAAGAGGCTGTGGATTAGGACATGAGACTAAATGAGAAATAG (SEQ ID
20 NO: 246)

AOLFR134 sequences:

- MTIILEVDNHTVTTRFILLGFTRPAFQLLFFSIFLATYLLTLENLLJLAIHSDGQLHKPMYFFL
SHLSFLEMWYVTVISPKMLVDFLSHDKSIFNGCMTQLYFVTVFVCTEYILLAIMAFDRYVAIC
25 NPLRYPVIMTINQLGCTAGGCWFCGLMTAMIKMVIAQLHYCGMPQINHYFCDSIPLNVSC
DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRPSAQGRQKAFSTCASHLTVVILFYSM
LFTYARPKLMYAYNSNKVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQNGAFS
(SEQ ID NO: 247)
- 30 ATGACCACATAATTCTGGAAGTAGATAATCATACTGACAAACAGTTTCATTCTCTG
GGTTTCCACACGACCAGCCTTCCAGCTCTCTTTTCTCCATTTTCTGGCAACCTATCTG
CTGACACTGCTGGAGAATCTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCATGTACTTCTTGTAGCCACCTCTCCTTCTGGAGATGTGGTATGTACAGTCACTC
AGCCCCAAGATGCTTGTGACTTCTCAGTCATGACAAGAGTATTTCTCTCAATGGCTGCA
35 TGACTCACTTTACTTTTTTGTGACCTTTGTCTGCACTGAGTACATCCCTCTTGCTATCAT
GCCTTTGACCGCATGTAGCCATTGTAAATCCACTACGCTACCCAGTCATCATGACCAACC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTA
GATGGTTTTTATAGCAACAATCTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGT
ATATCTCTCCACTCTTAAAGCTCTCTGTGAGGATGCCTCAGAGGCTGAGATGGTGGACTT
40 CTCTTGGCCCTCATGGTCATGCTATCTCTTTGTGTGTGGTGGCATCTCAGCTGCTA
TCTTGTCCACCATCTCAGGATCCTTCTGCTCAGGGCCGCCAAAAGGCATTTCTCCACCTG
TGCTGCCCACTGACCGCTGTAATCTCTTCTATCCATGACACTTTTCACTATGCGCTC
CCAAACTCATGTATGCTCAACAATCCAAACAAAGTGGTATCTGTTCTCTACACTGTCATTG
CCACTCTCAACCCCATCAATTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
45 AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAATGGGGCTTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

- MIFPSSHDSQAFSTVDMVEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIR
DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASVSEDKRISLAGCGAQLFFSCVVAYTECYLL
50 AAMAYDRHAICNPLLYSGMTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIDHFFC
DAPPLVKMSTCTNRVYEKVLGVVGTFLSSILAILISYVNILLAILRIHSAASGRHKAFTSCASH
ISVMLFYGSLFLMYSRPSSYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFKATQTIQPQ
T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTACCTCCGTGGACATGGAAGTGGGAAAT
GCACCATCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCAGTGGGACCGCAT
TCTATTGGAGTGTTTCTGATGCTCTATTGATAACCTTGTACAGGAAACATGACCTTGGTTA
TCTTAATCCGAATGATTCACCTTGCATACACCTATGTACTTTTCATTGGCAATCTGTCT
5 TTTTGGATTCTGGTATACCTCTGTGTATACCCCAAAATCCTGGCCAGTTGTGTCTAGA
AGATAAGCCGATTTCCTTGGCTGGATGTGGGGCTCAGCTGTTTTTCTGTGTGTAGCT
ACACTGAATGCTATCTCTGGCAGCCATGGCATATGACCCGCAATGCAGCAATTTGTAACCC
ATGTCTTTTTCAGGTACCATGTCCACCGCCCTGTGTACTGGGCTGTGTCTGGCTCTGTACA
10 TAGGAGGATTTTTGAATGCCATAGCCCACTACTGCCAATACATTCCGCCTGCATTTTGTGG
TAAAAATATCATTGACCACTTTTCTGTGATGCACCACTTGGTAAATAATGTCTGTGACA
AACACAGGCTTACGAAAAAGTCTGTGTGGTGTGGGGCTTCACGACTATCTCCAGCTA
TCTTGTCTATCTGATTTCCTATGTCAACACTCTCTGGCTATCTCTGAGATCCACTCAGCT
TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTATGCTCTTCTA
TGGATCATTTGTTTATGTATTCAAGGCCTAGTTCACCTACTCCCTAGAGAGGACAA
15 GTAGCTGCTTGTCTACACCGTGATCAACCCACTGCTCAACCTCTCATGTATAGGCTGAG
AACAAGATATCAAGAGGCCCTCAGGAAAGCAACACAGACTATACAACCACAAACATG
(SEQ ID NO: 250)

AOLFRI36 sequences:

20 MTMENYSMAAQFVLDLGLTQQAELQLPLFLLGIHYVTVVGNLGMILLIIVSPLHPTMYFFL
SSLSFGCTFYSSVITPKMLNVNFGKKNITLYSECMVQLFFVFFVVAEGLYLLTAMVADRYVAIC
SPFLYNAIMSSWCSLLVLVAFFLGLSALTHTSAMMKLSFCKSHIINHVFCDVPLNLNSCNT
HLNELLLFIAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCSHLMVAVIFFGSITFMY
FKPPSSNSLDQEKVSSVYFTTVPMLNPLIYSLRNKDVKKALKRVLVGK (SEQ ID NO: 251)

25 ATGACCATGGAATAATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAAACAGCAAG
CAGAGCTCCAGCTGCCCTCTTCTCTCTGTTCTCTGGGAATCTATGTGGTCACAGTAGTGGG
CAACCTGGGATGATTCTCTGATTGCAGTCAGCCCTCTACTTCACACCCCACTGTACTATT
30 TCTCAGCAGCTGTGCTTCTCGTCGATTTCTGCTATTCTCTGTGCTTACTCCCAAAATGCTG
GTGAACCTTCTAGGAAAGAAGAAATAACAATCTTACTCTGAGTGCAATGGTCCAGCTCTTT
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCTGACTGCCATGGCATATGATCGCTA
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCTCATGGGTCTCATGCTGC
TAGTGCTGCTGCTTCTTCTTGGGCTTTCTCTGCTGCTGACTCATCAAGTGCCATGATG
35 AAATGCTCTTTTGCAATCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCTCT
CAATCTCTCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTTATCATTGCGGGGTTA
ACACCTTGGTGCCCAACCTAGCTGTGTGCTGCTCTCATGCTTACGCTCTACAGCATCTT
CACATCCGCTCCAGAGGGCCGGTCCAAAGCTTTTGGAAACATGCACTCTCATCTCATGG
CTGTGGTGATCTCTTTGGGTCCATTACCTTCATGTATTCAAGCCCCCTTCAAGTAACCTC
40 CTGAGCCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCTT
TAATATACAGCTCAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA
AATGA (SEQ ID NO: 252)

AOLFRI37 sequences:

45 MSPENQSSVEFLLGLPIRPEQQAVFFALFLGMYLTTVLNLLIMLLIQLDLSHLHTPMYFFLSH
LALTDISFSSVTPKMLNMNMQTHLAVFYKGCISQTYFFIFADLDSFLITSMAYDRYVAICHP
HYATIMTQSQCVMILVAGSWVIACACALLHTLLAQLSFCDHIHPHYFCDLGAALLKSCSDTSL
NQLAIFTAAITAMLFFLCILVSYGHIGVTILQIPSTGICKALSTCGSHSVVITYRITGLYFLP
PSSNTNDKNILASVIYTAVTPMLNPFYISLRNKDIKALRKLKLSRSGAVAHACNLTLGG (SEQ
ID NO: 253)

50 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCTCTCTGGGCTCCCCATCCGGC
CAGCTGAGCCGCTGTGTTCTTCGCCCTGTCTCGGCGATGACCTGACCACGGTGTGGG
GAACCTGCTCATCATGTGCTCATCCAGCTAGACTTCACTTACACCCCACTGTACTTCT
TCTTACGACCATGGCCCTCACTGACATCTCCTTTTCACTCTGCTGCTGCTCAAGTGTG
55 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAGGGATGCATTTTACAGACATATT
TTTTCATATTTTTTGCTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT

- GTGGCCATCTGTCATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTCAATGC
TGTGGCTGGGTCTGGGTCTATCGCTTGTGCGTGTGCTCTTTTGCATACCCCTCCTCTGGCC
CAGCTTTCCTCTGTGCTGACCAATCATCCCTCACTACTTCTGTGACCTTGGTGGCCCTGT
CAAGTTGCTCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTACAGACGACATTGACA
5 GGCATTATGCTTCCATTCTCTGTGCATCTGGTTTCTTATGGTCACATTGGGTACCATCTCT
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA
GTGGTGAATCTATTATCGGACAATTATTGGTCTCTATTTTCTCCCCCATCCAGCAACAC
CAATGACAAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
10 TTCAATTACAGTCTGAGAAATAAGGACATTAAGGGAGCCCTAAGAAAACTCTTGAGTAGG
TCAGGCGCAGTGCTCATGCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

- MLNFTDVTEFILLGLTSRRWEQVLEFFIVLVVYIITVVGNIQMMLLIKVSPQLNSPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSDDKTISYADCLAQCFFIALVHVEIFLAAIAFDRTYVIGNPLLY
15 GSKMSRQV CIRLITFPPIYIGFLTSLTATLWYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY
TMLILAGINFTYSLTVIISYLFILIAILRMRSAEGRQKAFSTCGSHPTAVIIFYGLIFMYLRPTE
ESVEQGMVAVFYTTVPMNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)
- ATGCTCAATTTCACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTGCGGAAT
20 GGCAAGTCTCTCTCTCATCGTTTTCTTGTGGTCTACATTACCCGTGGTGGGCAATATC
GGCATGATGTTGTTAATCAAGGTCACTCTCAGCTTAACAGCCCATGTACTTTTCTCTCA
GTCACTTGTCAATTGTTGATGTGTGGTTTTCTTCCAAATGTCACCCCTAAAATGTTGGAATA
CTGTATACAGATAAAAAACAATTCTTATGCTGGCTGTTAGCACAGTGTCTCTCTTCTAT
TGCTCTTGCCATGTGGAATAATTTTATTCTGCTGCGATTGCTCTTGATAGATACACAGTGA
25 TTGGAATCTCTTGTCTTATGGCAGCAAAATGCAAGGATGTCTGATTTCAGTGATTAC
TTCCCTTACATTATATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
ACTCTGTGGAATAATGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCTGTGCGGGACCTTTGAAAAGAATATAACAATGCTCATCTGTGCGGCATCAACTTC
30 ACATATTCCCTGACTGTAAATATCATCTCTACTATTATCATCTCATTTGCCATTGTGCGAAT
CGCTTACGAGAGAAGGAAGGCAGAAAGGCCTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATCATATTCTATGTTACTCTGATCTTATGATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCAAGATGATCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 256)

AOLFR139 sequences:

- MGFPGLHSWQHWLSPLALLYLLALSANILILINKEAALHQPMMYFFLGILAMADIGLATTIMP
KILAILWPNKATISLLECAQMYAHCFAVAMESSFPVCMADRYVAICRPLRYPISITSEVPKAN
GFMALNRSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSCDRRINSINQVLLAWTLMGS
40 DLGLIISYALILYSVLKNSPEAAKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLNLV
HNVIPALNPMVYALKNELRQGLYKVLRLGVKGT (SEQ ID NO: 257)
- ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT
ACCTCTTAGCTCTCAGTGCCAACATCCTTATCTGTATCATCATCAACAAAGAGGAGCAGCAT
45 GCACCAAGCTATGTAATAATTCTGGGCATCTTGGCTATGGCAGACATAGGCTTGGCTACC
ACCATCATGCTCAAGATTTTGGCCATCTTATGTTTCAATGCTAAGACCATCAGTCTCTGCG
AGTGCCTTGTCTCAGATGTATGCCATACATTGCTTTTGGCCATGGAATCAAGTACCTTTGT
CTGCAATGGCTATTGATAGATATGTAGCCATTGTGCAACCCTACGATATCCATCAATCATC
ACTGAATCTTTGGTTTTTCAAAGCAAAATGGGTTTCAATGGCACTGAGAAACAGCCTGTGTCTCA
50 TCTCATGGCTCTGTGTGGCTGCCAGAGGCATTACTGCTCCAGAAATCAAAATGAGCAGT
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAAATCAATAGCATT
AACCAGTCTCTTTTGGCTTGGCACTCATGGGAAGTGACCTGGGTTTGATTATTTATCAT
ATGCTCTAATACTTTACTCTCTCTGAAGCTGAACCTCCAGAAAGTGCATCCAAAGCCTT
AAGTACCTGCACCTCCCACTCATCTTAATCCTTTCTCTACACAGTCACTATTGTGATTT
55 CCATTACTCGTAGTACAGGAATGAGAGTTCCTCTTATCCAGTCTACTTAATGTGTACA

CAATGTCAATCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAAGGAACCTCAGG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

- 5 MLTINKTDLIPASFLNGVPGLEDTQLWISFPFCMSYVVMVGNCLLYLIHYEDALHKPMYY
FLAMLSFTDLVMSSTIPKALCIFWHLKDIGDFDECLVQMFHHTFTGMESGVLMLMALDRYV
AICPYLRYSTLINPVIKAVGTATFLRGVLLIHPFTLTKRLPYCRGNILPHYTCGDMHMSVAKLSG
NVKVNAYIGLMVALLIGGFDILCTISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF
10 FSFSHRFGHEIHPSSCHIVANIVYLLPPTMNPVYGVKTKQIRDCVIRLSSGKDTKSYSM (SEQ
ID NO: 259)

- ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTATTCTGAATGGAGTCCAG
GACTGGAAGACACAACTCTGGATTCTCTCCCACTTCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCTCTACCTCACTTCACTATGAGGATGCCCTGCACAAACCCATG
15 TACTACTTCTTGCCATGCTTTCCTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCACTTCTTGTTTCATCTCAAGGACATTGGATTGTGAAATGCCCTGTGCCAG
ATGTTCTTCACTCCACACCTTCACAGGGATGGAAGTCTGGGGTGCTTATGCTTATGGCCCTGG
ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCTCCACCAATCCTGTAATT
20 GCAAGGTTGGGACTGCCACCTCTCGAGAGGGATTAATCACTATTTCCTTTTACTTCTTCT
CACCAGAGCCCTGCCCTACTGCAGAGGCAATATACTCCCCATACCTACTGTGAGCCACATG
TCTGTAGCCAAATTTGCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCGG
GCAGTGGTCAAGCTCTCTCAGCAGATGCTCGGCAGAAAGGCTTTAATACTGCACCTGCC
25 ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTCTCTCTCTTTCCCAACCGCTTTG
GGGAACACATAATCCCCCTTCTTGCCACATATTGAGCAATATTTATCTGCTCTACCA
CCCCTATGAACCTATTGTCTATGGGGTGAACCAACAGATACGAGACTGTGTCATAA
GGATCCTTTCAGGTTCTAAGGATACCAATCTCAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

- 30 MSSTLGHNMESPNTDVPVSFLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVVATEPVL
HKPVYFLCLMLSTIDLAAVSSTVPKLLAIFWCGAGHISASCLAQMFFIHAFCMMESTVLLAM
AFDRYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPLIGRLNFCQSHVILHITYCEHMA
VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTGCSHVC
35 VILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLPPLANPVPVYGVKTKQIRKRVVRVFGSQG
GMGIKASE (SEQ ID NO: 261)

- ATGTCCAGCACTCTTGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCTTCTG
TCTTCTTCTCTGGGCATCCAGGTCTGGAACAATTTCAATTGTGGCTCTCACTCGCTGTG
TGTGGCTTAGGCACAGCCAAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG
40 AACCACTTTGCACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCACTCAAGTGGCT
GCCTCTGTCTCCACAGTTCACAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
CTGCCTCTGCTGCTGGCACAGATGTTCTTCTATTCATGCTTCTGCATCTGAGGTCCACT
GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATTGCCA
CAATCCTCACTGACACCATCATGTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT
45 GCTCATGCTCCCAATGTCCTTCTTATTGGGCGTTTGAACCTTCTGCCAAAGCCATGTGATCC
TACACAGTACTGTGAGCAGATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAAGGCTTA
ACCGTGTGATGGGCTGACAGCTGCACTGTTGGTCAITGGGGTTGACTTGTTTGCATTGG
TCTCTCTATGCCCTAAGTGCAACAAGCTGTCTTCGCTCTCATCCCACTGAAGCTCGGTGCA
AGGCCCTAGGACCTGTGGTTCCCATGTCTGTGTCATCTCATCTTATACACCAAGGCTC
50 TTTCTCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATCTCTTTGGC
CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAA
AGATCCGTAAGAGATTGTGAGGTTGTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT
CTGAGTGA (SEQ ID NO: 262)

AO LFR143 sequences:

MLGLNGTFFQPATLQLTGIPGIQTGLTWVALIFCILYMSIVGNLSILTLVFWEPALHQPMPYYFL
SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVQMFFIHTFSFMESGILLAMSLDRFVAICY
PLRYVTVLTHNRILAMGLILTKSFTTLFPFPVVKRLPFCCKGNVLHHSYCLHPDLMKVACGDI
HVNNYIGLLVIIFTYGMDSFTILLSYALILRAMLVIISQEQRLKALNTCMSHICAVLAFYVPIIAVS
MIHRFWKSAAPPVVHVMSNVYLFVPPMLNPIIYSVKTKEIRKGILKFHKSQA (SEQ ID NO:
263)

ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAACATCCAGCTGACAGGCATTCTGT
GGATCAACAACAGGCCCTACCTGGGTTGCCCTGATTTCTGCATCCTCTACATGATCTCCATT
GTAGGTAACTCAGCAATTCTCACTCTGGTGTITTTGGGAGCCTGCTCTGCATCAGCCCATGT
ACTACTTCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTTCTACACTTCCCACT
GTGATTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCCTGGTCCAGAT
GTTCTTCATCCACACTTCTCCTTCATGGAGTCAAGGCATACGTCTGGCCATGAGCTTGGATC
GCTTTGTGGCTATTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
GCTATGGGTCTGGGCATCCTTACCAAGAGTTTACCACTCTCTTCCCTTTCCCTTTTGTGGT
GAAACGACTGCCCTTCTGCAAAGGCAATGTTTGCATCACTCCTACTGTCTCCATCCAGAT
CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA
TTTTTACCTATGGTATGGACTCAACTTTTCCTGCTTTCCTACGCATTGATCTCGAGAGCC
ATGCTGGTTCATCATCCAGGAACAGCGGCTCAAGGCCTCAACACCTGCATGTGACACACA
TCTGTGCAGTGCTGGCCTTTTATGTGCCCAATGTTGCTGTCTCCATGATTACCGCTTCTGG
AAAAGTGTCTCAACCTGTTGTTTCATGTATGATGTCCAATGTCTACCTGTTTGTACCCACCAT
GCTCAACCTTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
TTCCATAAATCCAGGCCTGA (SEQ ID NO: 264)

AO LFR144 sequences:

MGLFNVTHPAFFLLTGIPGLESSHWSLGPLCMYAAVALGGNTVILQAVRVEPSLHEPMPYYFL
SMLSFSDAISMATLPTVLRFTCLNARNITFDACLQMFILHFFSMMESGILLAMSFDRYVAICD
PLRYATVLTVEVIAAMGLGAAARSFITLPLPFLIKRLPICRSNVLSHSYCLHPDMMLACADISI
NSIYGLFVLVSTFGMDLFFIFLSYVILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
TVHRFGKHVPYCIHVLMNSVYLFVPPVNLPIYSAKTKEIRRAIFRMFHIIKI (SEQ ID NO: 265)

ATGGGGTTGTTCATGTCACTACCCCTGCATTCTTCTCCTGACTGGTATCCCTGGTCTGGA
GAGCTCTCACTCCTGGCTGTCAAGGCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
AATACAGTGATCCTGCAGGCTGTGCGAGTGGAGCCAGCCTCCATGAGCCCATGTACTACT
TCTGTGCTATTTGTCTTCACTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
CGAACCTTCTGCCTCAATGCCCGCAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT
TATTCATCTTCTTCCATGATGGAATCAGGATTTCTGCTGGCCATGAGTTTGTACCCGTATG
TGGCCATTGTGACCCCTTGGCGTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
GGGTTTAGGTGACGCTGCTCGAAGCTTCATCACCCCTTTTCCCTCTCCCTTTCTTATTAAGA
GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCTGCAACCCAGACATGATG
AGGCTTGCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTGTCTGTATCCAC
CTTTGGCATGGACCTGTTTTATCTTCTCCTCTATGTGCTCATTCTGCGTCTGTCAATGG
CAACTGTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTCACATATCTGGC
GTGATCTGCATTTTATGTGCCAATGATTGGGGTCTCCACAGTGACCCGCTTGGGAAGCAT
TGCCCATGCTTACATGATGCTCATGTCAAATGTGTACCTATTGTGCTCCTGTGCTCAAC
CCCTCTCATTTATAGCGCCAAAGACAAGGAAATCCGCCGAGCCATTTCGCGATGTTTAC
CACATCAAAATATGA (SEQ ID NO: 266)

0986055-062201

AOLFR145 sequences:

MSVQYSLSPQFMLLSNITQFSPIFYLTLSFPGLEGIKHWIFPFFFMVYMAISGNCFILIIKTNPRLH
TPMYLLSLLALTDLGLCVSLPTTMGIFWFSQSIFYGCAQIQMFCIHFSFMESSVLLMMSFD
RFVAICHPLRYSVIHTGQQVVRAGLIVIFRGPVATIPIVLLLKAFPYCGSVVLSHSFCLHQEVIQLA
CTDTTFNLYLGLMVVFTVMLDLVLIALSYGLIHVTVAGLASQEEQRRAFQTCTAHLCAVLV
FVPMGLSLVHRFGKHAPPAIHLLMANVYLVFVPMPLNPIIYSIKTKEIHRAIHLKLLGKKASK
(SEQ ID NO: 267)

- 10 ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
CCCCAATATTCATCTCACCAGCTTTCTCGGATTGGAAGGCATCAAAACCTGGATTTCATCC
CCTTTTCTTATGTACATGTTGCCATCTCAGGCCAATTGTTCAATTCTGATCAITTAAGA
ACCAACCTCGTGTGCACACCCCATGTACTATCTACTATCCTTGTCTGGCCCTCACTGACCT
GGGGCTGTGTGTGCCACGTGTGCCACCACTATGGGGATCTCTGTTTAACTCCCAGAGT
ATCTACTTTGGAGCGGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCCTTCATGGAGTC
15 CTCAGTGCTCCTCATGATGTCTTTGACCGCTTTGTGGCCATCTGCCACCCTCTGAGGTATT
CGGTCAATTCACCTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTGATCTCTCCGGGGACC
TGTGGCCACTATCCCTATTGTCTCTCTCTGAAGGCTTTTCCTACTGTGGATCTGTGGTCC
TGTCCTCACTATTTTGCTGCACCAAGGAAGTGATACAGCTGGCCTGCACAGATACCACTCT
CAATAAATCTGATGGACTGATGGTGGTAGTTTCACTGTGATGCTGGACCTGGTGCTCATC
20 GCTGCTCTATGGACTCATCTCGACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
GCCGTGCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCACT
ATGGGGCTGTCCCTGGTGCACCGTTTGGGAAGCATGCCCACTGCTATTGATCTTTAT
GGCCAAATGCTACCTTTTGTGCTCTCCATGCTTAACCAATCATATACAGCATTAAAGACC
AAGGAGATCCACCGTGCCTATATCAAACTCCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
25 ID NO: 268)

AOLFR146 sequences:

MSQVNTNTQEGIYFILDIPGFEASHIWISIPVCCLYTISIMGNTILTVIRTEPSVHQRMVFLSLM
LALTDLGLTTLPTVMQLWFNVRRISSEACFAQFFHLHGSFMESSVLLAMSVDYVAICCP
LHYASILTNEVIGRTGLAIHCCCVLAVLPSLFLKRLPFCCHSHLLRSYCLHQDMIRLVCDIRLN
SWYGFALALLIIVDPLLIIVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSM
T
HRFAKHASPLVHVIMANIYLLAPPVMPNPIIYSVKNKIQIWGMLNFLSLKNMHSR (SEQ ID NO:
269)

- 35 ATGTCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
GATTGTGAGGCCTCCCACATCTGGATCTCCATCCCGTCTGCTGTCTCAACACATCTCCATC
ATGGGCAATACCACCATCCTCACTGTCAATTCGCACAGAGCCATCTGTCAACAGCGCATGT
ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCCCTCACCACCCTACCCACA
GTACATGACGCTCTCTGGTTCACAGTTCGTAGAATCAGCTCTGAGGCGCTGTTTGTGCTAGTT
40 TTTCTTCTTCATGGAATCTCCTTTATGGAGTCTTCTGTCTCCTCGCTATGCTCGGTGACT
GCTATGTGGCCATCTGCTGTCCCTCCATTATGCTCCATCTCTACCAATGAAGTCATTGGT
AGAATCGGTTAGCCATCATTTGCTGCTGTGTTCTGGCGGTCTTCCCTCCCTTTTCTTACT
CAAGCGACTGCTTTCTGCCATCCACCTTCTCTCTCGCTCTATGCTCTCCACAGGATA
TGATCCGCTGGTCTGTGTGACATCAGGCTCAACAGCTGGATGGATTGCTCTTGGCTT
45 GCTCATATTATCGTGGATCCTCTGCTCATTTGATGCTCTCTATACTATTGCTGAAAATA
TCTGGGCACAGCCAGCTGGGCTGAGCGACTCGTCCCTCAATACTGCTGCTCCACAT
TCTAGCTGTCTGGTCTCTACATTTCCCATGGTGGTGTATCTATGACTCATCGCTTTGCCA
AGCATGCTCTCCACTGGTCCATGTATATCATGGCCAATATCTACTGCTGGCACCCCGGT
GATGAACCCCATCATTTACAGTGTAAAGAACAGCAGATCCAATGGGGAATGTAAATTT
50 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

MPSASAMIFNLSSYNPGPFILVIGPGEQFHVWIGIPFCIIYIVAVVGNCLLYLIVVEHSLHEPMF
FFLSMLAMTDLLSTAGVPKALSIFWLGAERTFPGCLTQMFFLHYNFVLDLSAILMAMAFDHYV
AICSPRLRYTTLTPKTIKSAMGISFRSFCILPDVFLTCLPFCRTRIPIHTYCEHJGVAQLACADISI
NFWYGFVCPIMTVISDVILAVSYAHILCAVGLPSQDACQKALGTGSHVCVILMFYTPAFFSI

LAHRFGHNVSRTHFIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO: 271)

5 ATGCCATCTGCCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT
TCTGGTAGGAGATCCCAAGGCTCGGAGCAATTCCATGTGTGGATTGGAATTCCTTCTGTATC
ATCTACATCTGTAGTCTGTTGGGAAACTGCATCCTTCTTCACTCATTTGTGTGGTGGAGCATA
GTCTTCATGAACCATGTGTTCTTCTTCTTCCATGCTGGCCATGACTGACCTCATCTTGTCC
ACAGCTGGTGTGCCATAAGCACTCAGTATCTTTGGCTAGGGGCTCGCGAAATCAACATTC
CAGGATGGCTTACACAAATGTTCTTCCCTTCACTATAAATTTGTCTGGATTGACCATTTCTG
10 ATGGCCATGGCATTTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATACCACCATCTT
GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTTCCGAAGCTTCTGCATATC
CTGCCAGATGATTTCTTGTGACATGCTCGCTTCTTGCAGGACACGCATCATACCCCA
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCTGTGCTGATATCTCCATCAACTCTGT
GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCT
15 ACGCACACATCTCTGTGCTGCTTGTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT
CGGCACCTGTGGTCTCATGTCTGTGTCATCCTCATGTTTATACACCTGCCTTTTCTCCA
TCTCTGCCCATCGCTTGGACACAATGTCTCTCGCACCCTCCACATCATGTTTGCCAACTC
TACATTGTTATCCCACTGCACCTCAACCCATGGTTTACGGAGTGAAGACCAAGCAGATCA
GAGATAAGGTATACCTTTGTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

20 **AOLFR148 sequences:**

MPTVNHSGTSHTVFHLLGIPGLDQHMWISIPFFISYVTALLGNSLLFIHLTKRSLHEPMLYFLC
MLAGDIVLSTCTIPQALAIWFRAGDISLDRCTQLFHHSTFISEGILLVMAFDHYIAICYPLR
YTITLINALIKKICVTVLSRYGTTFIPIHLLKRLTFCQNNIIPHTFEHIGLKYACNDIRINIWYG
25 FSLMSTVVDLVVILFISYMLILHAVFHMSPDACHKALNTFGSHVCIILFYGSGIFTILLQRFGR
HIPPCIHLPLANVCILAPMLNPIHYGIKTKQIQEQVVQLFIKQKITLV (SEQ ID NO: 273)

30 ATGCCTACTGTAAACACAGTGGCACTAGCCACACAGTCTTCCACTTGTGGGCATCCCTG
GCCTACAGGACAGCAGCATGTGGATTCTATCCCACTTCTCATTTTCCATGTACCCGCCCTT
CTTGGGACAGCCCTGCTCATCTTCTATTCTCTACAAGCGCAGCCTCCATGACACCATGT
ACCTCTTCCCTGTCATGCTGGCTGGAGCAGACATTGCTCTCCACGTCACCATTTCTCAG
GCCTTAGCTATCTTCTGGTTCGGTGTGGGGACATCTCCCTGGATCGTGTGATCACTACGCT
CTTCTTCCATCATTCACCTTCTCATCTCTGAGTCAGGGATTTGCTGGTGTGGGCTTTGACC
ACTATATTGCCATATGCTACCCACTGAGGTACACACCATCTTACAAATGCTCTGATCAA
35 GAAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT
TAAAAAGATTGACTTTCTGCCAGAATAATATATTCACACACCTTTTGTGAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTGCAATAAACATTTGGTATGGGTTTCCATTCTA
ATGTCGACGGTGGTCTTAGATGTTGACTAATTTTATTTCTATATGCTGATTTCTCCATG
TGCTTCCACATGCTTCTCCAGATGCTTGCCACAAAGCTTCAACACATTTGCTGCCATG
40 TCTGCATCATCTCTCTTTTATGGGTCTGGCATCTTCAATCTCTACCCAGAGGTTTGGG
CGCCACATTTCCACCTGTATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTAATTTATGGGATCAAAACCAAGCAATCCAGGAACAGGTGGTTCAGTTT
TGTTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

45 **AOLFR149 sequences:**

MSNASLLTAFILMGLPHALDAPLFGVFLVYVYVTLVGLNLLILVIRVDSHLHTMYFYFLTNL
SFIDMWSTVTVPKLLMTLVFSPGRAISFHSMAQLYFFHFLGGTECF.YRVMSCDRYLAISYP
LRYTSMMTGRSCTLLATSTWLSGLSHSAVQAILFHLPCYCGPNWQHLYLCPAPPIKLACADTS
AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSSEKGRHAFQTCASHCIVLVCFFGPGFLFIYLR
50 PGSRKAVDGVVAVFYTVLPLLPVYVYTLRNEVKKALLKLDKVAHSQSK (SEQ ID NO:
275)

55 ATGTCCAACGCCAGCCTACTGACAGCGTTATCTCTATGGGCCTTCCCATGCCACAGCGC
TGGAGCCGCCCTCTTGGAGTCTTCTGGTGGTTTACGTGCTCACTGTCTGGGGAACCT
CCTCATCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCATGTACTACTTCTCTCA
CCAACCTGTGCTTCATTGACATGTGGTTCTCCACTGTACCGGTGCCAAAATTGCTGATGAC

TTTGGTGTGCCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCATTTCT
 TTCACTTCTTACGGGGGACCGAGTGTTCCTCTACAGGGTTCATGTCTGTGATCGCTACCT
 GGCATCAAGTTACCGCTCAGGTACACAGCATGATGACGGGGCTCGTGTACTTCTG
 5 GCCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGCCAGGCCATATTGACTTTC
 ATTTGCCCTACTGTGGACCCAACCTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCTT
 GAAACTGGCTCTGTGCAGACACCTCAGCCATAGAGACTGTCAITTTTGTGACTGTGGATA
 GTGGCTCGGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGCTGTTCATCTCT
 GCGGATCCGCACTCAGAGGGGAAGCACAGAGCCTTCAGACCTGTGGCTCCACATGHTAC
 10 GTGGTCTTTGCTCTTTGGCCCTGGTCTTTTCATTACCTGAGGCCAGGCTCCAGGAAAGC
 TGTGGATGGAGTTGTGGCGTTTTCACACTGTGCTGACGCCCTTCTCAACCCTGTGTGT
 ACACCTGAGGAACAAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAGAGACAAAGTAGCAC
 ATTCTCAGAGCAAAATAG (SEQ ID NO: 276)

AOLFRI50 sequences:

15 MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTTLLGNLLIMVTVTCESLRHTPMYFLLR
 NLALDIFCSSTAPKVLDDLLSKKKTISYTSMTQIFLHLLGGADIFLSVMAFDYMAISKPL
 HYVTIMSRGQCTALISASWMMGFVHSIVQISLLLPFCGPNVLDIFYCDVPQVLKLTCTDTFA
 LEHLMISNGLVTTLWFIFLLVSYTVLMTLRSQAGGGRKKAISTCTSPHLLCGDPAALHCLC
 20 PALHCPPHRKHLCHLHCHLPSAEPDLHSEEPGNEVSHKTEEKTRAF (SEQ ID NO: 277)
 ATGGAGTTGGGAAATGTACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
 AAGACCAGAGTTTGGTCTTGTCTTTTATATGTCTGTGTACATGACGACTTCTGTGGGA
 AACCTCTCATCATGGTCACCGTGACCTGTGAGTCTCGCTTCACACCCCATGTACTTCTCT
 GCTCCGCAATCTAGCCATCTTGTACATCTGCTTCTCCTCCACAACCTGCTCCTAAGACTTGTG
 25 TGGACCTTCTGTCAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATTTTCT
 CTTCACCTCTTGTGGGGGACAGACATTTTTCTCTCTGTGTGAGCGTTGACTGCTACA
 TGGCCATCTCAAGCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
 CATCTCTGCCCTTGTGATGGGGGGCTTGTGCACCTCATCGTGCAGATCTCCCTGTGTGCTG
 30 CTCTCCCTTTCTGTGGACCAATGTCTTGAACATTTCTACTGCGATGTCCCCAGGTCCTC
 AAACCTACTTGCACTGACACTTTTGTCTGTGAGTTCTTGATGATTTCCAACAATGGCCCTGGT
 CACTACCTGTGGTTTATCTTCTGCTTGTGCTCAACAGTCACTCCTAATGACGCTGAGGT
 CTCAGGAGGAGGGGGGAGGAGGAAAGCCATCTCCACTTGCACCTCCCCACATCACTGTG
 GTGACCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCAC
 35 AGAAAAAGGCVCTCTGTACCTTCACTGTCACTCCCTCTGCTGAACCCCTTTGATCTACA
 CTCTGAGGAACCAAGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
 CTGA (SEQ ID NO: 278)

AOLFRI51 sequences:

15 MFSPNHTIVFILLGLTDDPVLEKILFVFLAIYLLTLNAGNLCMILLRTNSHLQTPMYFFLGHLS
 FVDICYSSNVTPNMLHNFLSEKQTISYAGCFTQCLLFIALVITEFYILASMLDRVYVICSPLHYS
 40 SRMSKNICVCLVTPYPMYGLSFGFSQSLTFHLSFCGSLNHFYCADPPLIMLACSDTRVKKMA
 MPVVAGFNLSLLFIHLLSYLFIFAIFRIRSAEGRHKAFTSCASHLTIVTLFYGTLCFMYVRPPE
 KSVEESKITAVFYTFPLSPMLNPLIYSLRNTDVLAMQQMIRGKSFHKIAV (SEQ ID NO: 279)
 45 ATGTCTCCCCAAACACACCATAGTGACAGAATTCATTCTCTGGGACTGACAGACGACC
 CAGTGCTAGAGAAGATCTGTTTGGGGTATTCCTTGGCATCTACCTAATCAACACTGGCAGG
 CAACCTGTGCATGATCTGCTGATCAGGACCAATCCCACTGCAACACCATGATTTCT
 TTCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTATCTCCAAATATGCT
 GCACAATTTCTCTCAGAACAGAAAGACCATCTCCTACGCTGGATGCTTCACACAGTGTCTT
 50 CTCTCATCTGCCCTGGTGATCACTGAGTTTACATCTTGTCTTCAATGGCATGGATCGCTA
 TGTAGCCATTTGACGCCCTTGTCAATTACAGTTCCAGGATGTCCAAGAATCTGTGTCTGT
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTCTCTCAGTCACTGTAACCTT
 TCACTTATCTCTCTGTGGCTCCCTTGAATCAATCATTTCTACTGGCTGATCTCTCTCTTA
 TCATGCTGGCTGCTCTGACACCGGTGCAAAAGATGGCAATGTTTGTAGTTGACAGGCTT
 55 TAATCTCTCAAGCTCTCTTCATCATTTCTTCTGTCTATCTTTTCATTTTTCAGGCAATCT
 CAGGATCGTGTCTGTAAGGCAGGCACAAGCCTTTCTACGTGTCTTCCACCTGACA

ATAGTCACCTTTGTTTTATGGAACCCCTCTTCTGCATGTACGTAAGGCCCTCCATCAGAGAAGT
CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTGTAGGCCAAATGCTGAACCC
ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
AAATCCTTTCATAAAATTGCAGTTAG (SEQ ID NO: 280)

AOLFR152 sequences:

MDQNHNTNVKEFFLELTRSREFFLVVFFVAVVYATVLGNALIVVTITCESRLHTPMYFLLRN
KSVLDIVFSSITVPKFLVDLLSDRKTISYNDCAQIFFHFHAGGADIEFLSVMAYDRYLAIAPL
HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPPFCGPNLTDAFYCYVLQVVKLACTDT
FALELFMISNNGLVTLWFLLLLSYTVILVMLRSHSGEGRNKALSTCTSHMLVTVLHFVPCV
YIYCRPMTLPMDDTISINNTVITPMLNPIIYSLRNQEMKMSAMQRLQRRLPSESERKVG (SEQ ID
NO: 281)

ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTCTCGAACTTACACGTTCCT
GAGAGCTGGAGTTTTTCTTGTTTGTGGTCTCTTTGCTGTGTATGTAGCAACAGTCTCGGG
AAATGCATCTATTGGGTCACTATTACCTGTGAGTCCCGCTACACACTCCTATGTACTTTC
TCTCGGGCAACAAATCAGTCTCGGACATCGTTTTTTCATCTATACCCGTCCCAAGTCTCGT
GTGATCTTTTATCAGACAGGAAACCATCTCTACAATGACTGCATGGACAGATCTTTT
TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC
CTTGCAATCGCCAAAGCCCTGCATATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC
TTGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGAGTCTCAATCATCAGGTAATTCGATGC
TCCATTCTCCCTCTGTGGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
GTAAACCTGGCTGCACGTGACACCTTTGCTTTGGAGCTTTTCAATGATCTCTAACAAAGGCAT
TGGTGACCTGCTCTGGTTCTCTGCTCTGGGCTCTACACTGTCATCTGGTGATGCTG
AGATCCCACTTGGGGAGGGCGGAACAAGGCCCTCTCCAGTGCACGTCGCCCATGCTGTG
GTGGTGACTTCTCACTTCGTGCCTGTGTGTTACATCTACTCGCGGCCCTTCATGACGCTGCC
CATGGACACAACCATATCAATTAATAACACGGTCATTACCCCATGTGTAACCCCATCATC
TATTCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAAGAGGCTGCAGAGGAGACTTGGG
CTTCCGAGAGCAGAAATGGGGGTGA (SEQ ID NO: 282)

AOLFR153 sequences:

MSKTSLVTAFLITGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTPVKMLMTLVSPSGRAISFHSVAQLYFFHFLGSTEFLYTVMSYDRYLAIISYPL
RYTSMMSGRCALLATSTWLSGSLHSAVQTILTFHLPYCGPNQIHYLCDAPPILKLACADTSA
NEMVIFVDIGLVSAGCELLIVLSYVSIVCSILRIHTSEGRHRAFTCTASHCIVVLCFFVXCVFIYLR
PGSRDVEDGVVAIFYTVLTPLLNPVYVTLRNKEVKAVLKLKRDKVAHSQGE (SEQ ID NO:
283)

ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCTCACGGGCCTTCCCCATGCCCAAGGGC
TGGACGCCCACTCTTTTGGAACTTCTCTGGTGTTCAGTGTCTAGTGTCTGGGGAACCT
CCTCATCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCA
CCAACCTGTCTCTATTGACATGTGGTCTTCCACTGTCACGGTGGCCAAAATGCTGATGAC
CTTGGTGTCCCAAGCGGCAGGGCTATCTCTTCCACAGCTGGTGGCTCAGCTCATTTT
TCCACTTCTGGGGAGCACCAGTGTTTCTCTACACAGTCAATGTCCTATGATCGTACTTGT
GCCATCAGTTAACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGTGTGCCTCTGTG
CCACAGCACTTGGCTCAGTGGCTCTGCACTCTGCTGTCCAGACCATAITGACTTCCAT
TTGCCACTGTGGGACCAACAGATCCAGCACTATTGTGTGATGACACCGCCCATCTGA
AACTGGCCTGTGACACACCTCAGCCAACGAGATGGTCATCTTTGTGGCAATTGGGCTAGT
GGCCTCGGGCTGCTTTCTCTGATAGTGCTGTCTTATGTGTCATGCTGTGTCATCTGCG
GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTCAGACACTGTGCTCCCATCGATCGT
GGTCCTTTGCTTTTTGTGNNCCGTGTGTTTTCATTACTGAGACAGGGCTCCAGGGACGTG
TGGATGGAGTGTGGCAGATTCTTACACTGTGCTGACACCCCTTCTCAACCCGTGTGTGTAC
ACCTGAGAAACAAGGAGGTGAAGAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
TCTCAGGGAGAAATA (SEQ ID NO: 284)

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMEsrNQSTVTEFIFTGPQQLQDGSLLYFPPLLFYTHIIDNLLIFSARL
DTHLGNPMYNFISIFSLFIWYTTATIPKMLSNLISEKKAISMTCILQMYFFHSLENSEGILLTT
MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGLJILLPEIVMISTLPFCGPNQHQIFCDLVP
VLSLACTDTSMILEDVIAHVTHITFLIALSYVRIVTVLIRPSSSEGROKAXSTCAGHLMVFLIFFG
SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFNFNPIIYSLRNKDMNNAIKKLFCLQKVLNKPGG
(SEQ ID NO: 285)

- 10 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
CCTGTACTTCTTCTCTTACTTTTCACTCATATACTTTATATCACTTGATCACTTAATATCTT
CTCTGCTGTAAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
CCTTTCTGGAGATCTGGTACACCACAGCCACCATTTCCAAGATGCTCTCCAACCTCATCAG
TGAAGAAGAAGGCCATCTCAATGACTGGCTGCATCTTGCAGATGTATTTCTTCCACTCACTT
15 GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATTCGA
ACCTCTTCGCTATCAAATGATCATGACCCCCGGCTCTGTGCTCACCTCTCTGCAGTTCC
TGCTCTTCGGTTTCTTATCTGCTTCCCGAGATTGTGATGATTTCCACACTGCCTTTCTGT
TGGGCCAACCAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
ACAGACACGTCCATGATTCTGATTGAGGATGTGATTCATGTGCTGTGACCATCATCACTTACTT
20 TCTTAATCATTGCCCTGTCCATTGTAAAGATTGTCACTGTGATATTGAGGATTCCTCTTCT
GAAGGAGGCAAAAGGCTNTTCTACCTGTGACGGCCACCTCATGCTTCTTCTGATATTTCT
TTGGCAGTGTCTCACTCATGTACTTGCCTTTCAGCAACACTTATGCCACCGTTTGGACAC
AGCCATTGCACTGATGTTTACTGTACTTGTCTCCATTCTTCAATCCCATCATTTATAGCCTGA
GAAACAAGGACATGAACAATGAATAAAAACTGTTCTGTCTCAAAAAGTGTGAACA
25 AGCCTGGAGGTTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTAAPQQLLIGISNYPQWRDTFFTLVLIIYSLTLNGFMIFLIHFDPNLHTPIYFFLSNL
SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLAAAMAYDRVVAISNP
LRYSVVMNPGVCVCLVATSWGTSLSVLTAMLRLRHFGGANVDHFAEILSLIKLTCSDTSL
NEFMILITSIFTLTLLPFGFVLLSYIRIAMAIRISLQGRKFAFTTCGSHLTVTVTIFGSAISMVYMKT
QSKSSPDQDKFISVFYGALTPMLNPLIYSLRKKDVKRAIRKVMVKRT (SEQ ID NO: 287)

- 35 ATGGCCATGGACAATGTCACAGCAGTGTTTCAAGTTTCTCCTTATTGGCATTCTAACTATCC
TCAATGGAGAGACACGCTTTTTCACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
AATGGATTATGATCTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
CCTTAGTAACCTGCTCTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
TGCATTGTTTCTTACCACCTCCCTACCTCTTATCCCGATGTTTGGCTCAACAGAGTGTG
TCTTTGGCTTTGGCCACAGCAGAGTGCTCTTACTGGCTGCCATGGCCTATGACCGTGTGG
40 TTGCTATCAGAACATCCCTGCGTTATTAGTGGTTATGAATGGCCACGTGTGTCTGCTT
GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCTATCCCTGAGG
CTTCACTCTGTGGGGCTAATGTCAACAACATTTTGCTGTGAGATTTCTCTCTCCATTAA
GCTGACCTGTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGATCTTCACTACC
TGCTGTACTACCATTTGGGTTTGTCTCTCTCTACATACGAATTGCTATGGCTATCATAAAGG
45 ATTGCTCACTCCAGGGCAGGCTCAAGGCTTTACACATGTGGCTCTCACTGACCGGTGG
TGACAATCTTATGGGTGAGCCATCTCCATGTATAGAAACCTCACTCAAGTCTCTCCCT
TGACCAGGACAAAGTTTATCTCAGTGTTTATGAGAGCTTTGACACCATGTGTGAACCCCTG
ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAGG
ACATGA (SEQ ID NO: 288)

50

AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPIFLMLFLSMYLATMLGNLLIILAVNSDSHLHTPMYFLLSI
LSLVDFICTSTTMPKMLVNIQAQOSINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP
LRYNVIMNPKLCGLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFFCELALHKLACSDVILN
55 NILVYLTVLGGVPLSGHFSYTRIVSVMKIPSAAGGKYKAFCISGSHLIVSVLIFYGTGFGVYLS
GATHSSRKGAALASVMYTVVTPMLNPLIYSLRNKMDMLKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATGTGTCAGGGGATC
CGGAGCTGCAGCCCATCTCTTCATGCTGTTCTGTCCATGTACCTGCCACAATGCTGGG
5 GAACCTGTGTCATCATCTCTGGCCGTCAACTCTGACTCCCACTCCACACCCCCATGACTTCC
TCTCTCTATCTGTCCTTGGTCGACATCTGTTTCACTCCACCACGATGCCCAAGATGCTG
GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGGTGCCTCACCCAAATCTGCT
TTGTCTCGGTTTTTTGTGGATTGGAATAATGGAATTCTGGTCATGATGGCCTATGATCGATT
TGTGGCCATCTGTGCACTGAGGTACAATGTCAATCATGATGAACCCCAAACTCTGTGGGCTG
10 CTGCTTCTGCTGTCTTCATCGTTAGTGTCTGGATGCTCTGCTGCACACGTTGATGGTGTCT
ACAGCTGCACCTCTGCATAGACCTGGAAATTCGCCACTTTTCTGTGAACTAGCTCATATTTC
TCAAGCTGCCTGTTCTGATGTCCTCATCAATAACATCCTGGTGATTTTGGTGACAGCCGCT
GTTAGGTGTTGTTCTCTCTCTGGGATCATTCTTCTACACACGAATTGTCTCTCTGTCA
TGAATAATCCATCAGCTGGTGGAAAGTATAAAGCTTTTCCATCTGCGGGTCACATTTAAT
15 CCGTGTTCCTTGTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
CCTCCAGGAAGGGTGAATAGCATCAGTGATGTATACCGTGGTCAACCCCATGCTGAACCC
ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAACTAATATCTAG
GATACCATTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

20 MGRNQATVSEFLLMKVTEDEPELKLIPFSLFSLMYLVTILGNLILLAVISDSHLHTPMYFLFN
LSFTDICTLTTTVPKILVNIQAQNSITVTGCLTQICLVLVFAGLESCFLAVMAYDRYVAICHPL
RYTVLMNVHFWGLLILSMFMSTMDALVQSLMVLQLSFCKNVEIPFCEVVQVILACSDTL
INNILYFASSVFGAIPLSGHIFSQIVTSVLRMPARSARGKYKAFSTCGCHKLVPSFLYGTAFGVYIS
SAVAESSRITAVASVMYTVVPQMMNPFYSLRNKEMKKALRKILGRLPFF (SEQ ID NO: 291)

25 ATGGGACCCAGAAACCAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC
CCAGAACTGAAGTTAATCCCTTTCAGCCTGTCTCTGTCCATGTACCTGGTCCACCATCTGG
GGAACCTGCTCATTTCTCTGGCTGTGATCTCTGACTCCACCTCCACACCCCCATGACTTCT
30 CTCTCTTTAATCTCTCTTTACTGACATCTGTTTAAACCAACACACAGTCCCAAAAGATCTT
AGTGAACATCCAAGCTCAGAAATCAGAGTATCACTACAGGCTGCTCACCCAGATCTGT
CTTGCTCTGGTTTTTGTGGCTTGGAAAGTGTCTTCTTGCACTCATGGCCTACGACCGCTA
TGTGGCCATTGTGCCACCACTGAGGTACACAGTCCCTCATGAATGTCCATTCTTGGGGCTTG
35 CTGATTCTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT
GCAGCTGTCTCTTCGAAAAACGTTGAAATCCCTTTGTTCTCTGTGAAGTCGTTCAAGGTC
ATCAAGCTCGCCTGTCTGACACCTCATCAACAACATCCTCATATATTTTGAAGTAGTGT
ATTTGGTGCAATTCCTCTCTCTGGAAATAATTTCTCTTATCTCAAAATAGTCACTCTGTTCT
TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACTGTGGCTGTCACTCTC
40 TGTTTTTCTTGTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTGTGCTGAGT
CTTCCGAATTACTGCTGTGGCTTCACTGATGTACACTGTGGTCCCTCAAATGATGAACCC
CTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAACTTATTGGTAG
GCTGTTTCTTTTATG (SEQ ID NO: 292)

AOLFR160 sequences:

45 MPMQLLLDPIHSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFSLMYLVTILGNLILL
AVISDSHLHTPMYFLFSLNLSFLDICTLSTTIPKMLVNIQAQNSRITSVGLTQICFVFFAGLENC
LLAAMAYDRYVAICHPLRYTVIMNPRCLGLLILLSLTTSVVNALLSLMVLRLSFCTDLEIPFF
CELAQVQLTCSDTLNNILYFAACIFGGVPLSGHILSYTQITSCVLRMPASGKHKAVSTCGSHL
SIVLLFYGAGLVYISSVVTDSPRKTAVASVMYSVFPQMVMNPFYSLRNKMDKMTLIRKFIGRIP
SLLWCAICFGFRFLE (SEQ ID NO: 293)

50 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTCCATCAGATTTCATCATCAACAG
CATGGAAGCGAGAAACCAACAGCTATTTCAAAATTCCTTCTCTGGGACTGATGAGAGAT
CCGGAACCTGCAGCCGCTCTTTTCAGCCTGTCTGTCCATGTACTTGGTCAACCATCTGGG
55 GAACCTGCTCATCTCTTGGCTGTCTCTGACTCTCACTCCACACCCCATGCTACTTCT
TCCTCTCCAATCTCTCTTTTGGCAATTGTTTAAAGCACAACACGATCCCAAAAGTGTGCT
GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCACCCAGATCTGCT

TTGTCCTTGTTTTTGTCTGGCTTGGAAAATTGTCTCCTTGCAGCAATGGCCCTATGACCGCTAT
 TGGGCCATTGTGCACCCCTTAGATACACAGTCATCATGAACCCCGCCTCTGTGGCCTGCT
 TGATTCCTCTCTCTCTGTGACTAGTGTGTGAATGCCCTTCTCTCAGCGCTGATGGTGTG
 AGGCTGTCTCTTGCACAGACCTGGAATCCCGCTCTCTCTGTGAATGGCTCAGGTCA
 5 TCCCACTCACCTGTTACAGACACCTCATCAATAACATCTGATATATTTGACGCTTGACATA
 TTTGGTGGTGTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT
 GAGAAATGCCATCAGCAAGTGGAAAGCACAAGCAGTTTCCACCTGTGGGTCTCACTCTCC
 ATTGTCTCTTGTCTATATGGGGCAGGTTGGGGGTGTACATTAGTCTCTGGTACTGACTC
 10 ACCTAGGAAGACTGCAAGTGGCTCAGTGATGATTCTGTGTCCCTCAAATGGTGAACCC
 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGAACCTTGAGGAAGTTCATAGGAGG
 ATACCTTCTCTCTGTGGGTGTCATTGTCTTGGATTACAGTTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

15 MEPRNQTSAQFILLGLSEKPEQETLLFSLFFCMYLMVMVGNLLILALISIDSHLHTPMYFFLANL
 SLVDFCLANTNTPKMLVSLQTGSKAISYPCCLLQMYFFHFFGIVDSVIIAMMAYDRFVAICHPLH
 YAKIMSLRLRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLPILRLSCTDTSVNR
 IFILIVAGMVIATPFVICLASYARILVAIMKVPASAGGRKKAFTSCSSHLVVALFYGTGTGVYLCF
 SSVLTIVKEKASAVMYTAVTPMLNPFYSLRNRDLKGLARKLVNRKITSSS (SEQ ID NO: 295)

20 ATGGAACCAAGAAACCAACCAAGTCATCTCAATTATCCTCCTGGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTTCTCTTTCCCTGTTCTCTGCATGTACCTGGTCATGGTCGTGGG
 GAACCTGCTCATCTCCTGGCCATCAGCATAGACTAGCTCCACCTCCACACCCCATGTACTTCT
 TCTGGCCAACTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCATAAGATGCT
 25 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCTGATCCAGATGTAC
 TTTCTCAATTTCTTGGCATCTGGACAGCGTCATAATGCCATGATGGCTTATGACCGGTT
 CGTGCCCATCTGCCACCAATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTTCGCCTG
 CTGTGGCGCGCCCTCTGGGCGTTTCTGTCTCATCTCACTCACTCACTCCCTCCTGATGGC
 30 CCGTCTCGTTTCTTGGCGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
 TCCGACTTCTGTGACGGACACCTCTGTGAATAGGATCTTCATCTCATTTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTGTGGCCATCA
 TGAAGGTCCCTCTGCAAGCGCGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACTGTC
 TGTGGTTGCTCTCTTCTATGGGACCACCAATTGGCGTCTATCTGTGTCCTCCTCGGTCTCA
 35 CCACGTGTAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCAACCCCATGTGTAATCC
 CTTCACTCAAGGAGTGTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACTCATCTTCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

40 MMRMLKEVRGRNQTEVTEFLLGLSDNPDQGVLFALFLIYMANMVGNLGMIVLIKIDLC
 LHPMYFFLLSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAGFYFFGSFLGTECFLLAMMA
 YDRIAIIWNPILLYPVLVSGRICFLIIATSLFAGCGNAAIHTGMTFRLSFCGRNINHFYCDTPPL
 LKLSCSDFHNGIVIMAFSSFIVISCVMIVLISYLCIFIAVLKMPSELEGRHKAFSTCASYLMAVTF
 FGTLFMYLRPTSSYSMEQDKVVSVFYTVIIPVLNPLIYSLKKNKDVVKALKKILWKHIL (SEQ ID
 NO: 297)

45 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC
 CTCTAGGACTTTCGACAAATCCAGATCTACAAGGAGTCCCTTTGCAATTGTTTCTGTTGAT
 CTATATGGCAAAACATGTGGGCAATTTGGGGATGATTGTATGTATAAGATGATGATCTGCT
 50 CTCACACCCCATGTATTTCTTCTCAGTAGCCTCTCTTTGTAGATGGCTCTTACTCTCTCT
 TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCAAT
 GATGTGCTGCCAGTTTCTACTTCTTTGGCTCCTTCTGGGGACTGAGTGCTTCTGTGGCC
 ATGATGGCATATGACCGCTATGACGCCATTGGAACCCCTGCTCTACCCAGTTCTCTGTTG
 CTGGGAGAAATTGCTTTTGTCTAATAGCTACCTCTTCTAGCAGGTGTGGAAATGGCAGC
 55 CATACATACAGGGATGACTTTAGGTTGTCTTTTGTGGTTCTAATAGGATCAACCAATTGT
 ACTGTGACACCCGCCCATGCTCAAACTCTCTTGTCTGATACCCACTCTCAATGGAGTGTG
 ATCATGGCATTTCTCAAGTTTATTTGTCATCAGCTGTGTTATGATTGTCTCATTTCTCACTCT

GTGTATCTTCATTGCCGCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAAGCCCTCTCC
 ACCTGTGCCTCTTACCTCATGGCTGTCACCATATCTTTGGAAACAATCTCTCATGTACTT
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTGTCTCTGTCTTTTATACAGTA
 ATAATCCCTGTGCTAAATCCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC
 5 TAAAGAAGATCTTATGGAAACACATCTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

MQRSNHVTVEFILLGFTTDPGMQLGLFVVLGVSLTVVGNSTLIVLICNDSCLHTPMYFFTGN
 10 LSFLLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
 LYAQAAMSIKLCALLVAVSYCGGFINSIIKKTFSENFNFRENIDDFCDLLPLVELACGEKGGYK
 IMMYFLLASNVICPAVLILASLYFIITSVLRISSSKGYLKAFSTCSSHLTSVLYGSLIYIALPRS
 SYSFDMDKIVSTFYTVFVPMNLNMIYSLRNKDVKEALKLLP (SEQ ID NO: 299)

ATGCAGAGGAGCAATCATACAGTGACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA
 15 GGAATGCAGCTGGGCCCTCTTCGTGGTGTTCTGGGCGTGTACTCTCTCACTGGTAGGAA
 ATAGACACCTCATCGTGTGTATCTGTAATGACTCCTGGCTCCACACACCCATGTAATTTTTC
 ACTGGAAATCTGTCTGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAGATCTCTAGT
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGTCTGGCTGCGCTGTGTCACTTCTCTCT
 20 CTGCAGGGCTGGCCTATAGTGAAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
 GGCCATCTCCAAGCCCCCTGCTTTATGCCAGGCCATGTCCATAAGCTGTGTGCAATTGCTG
 GTAGCAGTCTCATATGTGGTGGCTTTATTAACCTCTCAATCATCACCAAGAAAACGTTTTTC
 CTTAACTCTGCGCGTAAAAACATCATTGATGACTTTTCTGTGATTGCTTCCCTTGGTGG
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTCTCGTGGCCCTCAA
 25 TGTCACTCTGCCCGGAGTGCTCATCTGGCCCTCTACCTCTTTATCATCACCAGTGTCTTGA
 GGATCTCTCTCTCAAGGGCTACCTCAAAGCCTTCTCCACAGTCTCTCCACCTGACCTCT
 GTCACCTTTATACTATGGCTCCATTCTTACATCTACGCTCTCCCCAGATCTAGCTATTCTT
 TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATCTCCCATGTGTGAATCTCATG
 30 ATCTACAGCCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAAGCTTCTCCCATAA (SEQ
 ID NO: 300)

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFS DYLELQIPLFFVFLAVYGFVSVGNLGMIVIIKINPKLHTPMYFFLN
 HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFCFTFVVTLELFAVMAYDHFVAICNP
 35 LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSAKLSFHGFNTINHFCELSLSISYPDSYL
 SQLLFTVATFNEISTLILITLSYAFIIVTTLKMPSASGHRKVFSFCASHLTATIFHGTILFLYCVF
 NSKNSRHTVKVASVFYTVVIPLLNPLYSLRNKDVKDAIRKIINTKYFHIKHHYWFNFVIEQ
 (SEQ ID NO: 301)

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTCTTGGGCTTCTCAG
 40 ATTACCTGGAACCTCAAAATTCCCCTCTTCTTTGTATTCTGGCAGTCTACGGCTTCAGTGTG
 GTAGGGAATCTTGGGATGATAGTGATCATCAAAATTACCCAAATAGCCATACCCCATGT
 ATTTTCTCAACCAACCTCTCCTTTGTGGATTCTGCTATTCCTCATCATCTGCTCCATGA
 TGCTGGTGAACCTGGTGTGATAGAAGATAGAACCATTCTCTCAGGATGTTTGGTGCAATT
 CTTTTCTTTTGCACCTTTGTAGTGAAGTGAATTAATTCTATTGCGGTGATGGCCTATGACC
 45 ACTTTGTGGCAATTGCAATCCTCTGCTCTACACAGTTGCCATCTCCAGAACTCTGTGGC
 ATGCTGGTGGTGTATTGTATGCAATGGGGAGTGCATGTTCCCTGACACTCGCGTGCTCTG
 CTTTAAAGTTATCTTTTATAGTTTCAACACAAATCAATCATTCTCTGAGATTCTCTCC
 CTGATATCACTCTCTTACCTGACTCTTATCTCAGCCAGTTGCTCTTCTTCACTGTTGCCAC
 50 TTTTAAAGATAGAAGCACACTACTCATCTTCTGACATCTTATGCAATCATCATTTGACACCA
 CCTGAAGATGCCTTCAAGCAGTGGGACCCGCAAGTCTTCTCCAGTGTGCTCTCCACTCT
 GACTGCCATACCATCTTCCATGGCACCCTCTCTCTCTACTGTGTACCAACTCCAAAA
 ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTACACCGTGGTGAATCCCTTGTGAA
 TCCCTGATCTACAGTCTGAGAATAAAGATGTGTAAGGATGCAATCCGAAAAATAATCAAT
 55 ACAAATAATTTTCATATTAACATAGGCATTTGGTATCCATTAAATTTGTTATTGAACAATA
 A (SEQ ID NO: 302)

000005-06201

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLMLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
SNLSFLDICVYSSTAPKMLSDIITEQKTSIFVGCATQYFVFCGMGLTECFLLAAMAYDRYAACN
PLLTYLVLSHTLCLKMVMVGYVVGFLSSFIETYSVYQHDFCGYPYMINHFCDLPPVLALSCSDTF
TSEVVTFIVSVVVGIVSVLVVLSYGYVAAVVKISSATGRTKAFSTCASHLTAVTLFYSGSFFM
YMRPSSSYSLNRDKVVSIFYALVIPVVPNIISFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
(SEQ ID NO: 303)

- 10 ATGGCTGTAGGAAGGAACACACAAATTGTGACAAAATTCATTCTCCTGGGCACTTTCAGACC
ATCTCAAATGAAGATTTCCTTTTCATGTTATTTCTGGGGCTCACTCTGACGTTGGCC
TGGAACTTAAGCCTCATTGCCCTCATTAAGATGGACCTCACTGCACATGCCATGTACT
TCTTCTCAGTAACCTGTCTCTCGGACATCTGCTATGTGTCTCCACCGCCCTAAGATG
CTGTCTGACATCATCACAGAGCAGAAAACCAATTCCTTTGTGGCTGTGCCACTCAGTACT
15 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTCTCCTCGGACATATGGCCTATGACCC
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCATACACTTTGTTAA
AGATGGTGGTTGGCGCTATGTGGGTGGATTCTTCTAGTCTTTCATTGAAACATACTCTGT
CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTCTGTGACCTCCCTCCAG
TCTGGCTCTGTCTGCTCTGATACCTTCACCGAGCGAGGTGGTGACCTTCATAGTCAGTGT
20 GTGCGTTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGTGT
TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTTCACCTG
ACTGCTGTGACCTCTTCTATGGTTCTGGATTCTCTAGTCATGACGACCCAGCTTCAGTCA
TCCCTAAACAGGGACAGGTGGTGTCCATATTTCTATGCTTGTGATCCCCGTGGTGAAT
30 CCCATCATCTACAGTTTATAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGA
AGGACCCCGGGATTCTCACGGTGGACCACTCATTTTATGACCTTGGGCTAA (SEQ ID
NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFIFLGLTQNREVSLLVFLFLLVYVTTLLGNLLIMVTVTCESRLHPTMPYFLLH
NLSIADICFSSITVPKVLVDLLSERKTISFNHCFQMFLEHLIGVDFVSLVSMALDRYVAISKPL
HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLPLPFCGPNVDTFYCDVHRVLKLAHDIFIL
ELLMISNGLLTLLWFELLVSYIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIVYARP
FTALPMDKAIISVTFVISPLNLIYTLRNHEMKSAMRRLKRLVPSDRK (SEQ ID NO: 305)

- 35 ATGGAGATGGAAGAATGCACCAGGGTAAAGAATTTATTTCTCTGGCCTGACCCAGAATC
GGGAAGTGAGCTTAGTCTTATTTCTTTCTACCTCTGGGTATGTGACAACCTTGTCTGGGA
AACCCTCATCATGGTCACTGTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTT
GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTCCATCACAGTGCCCAAGGTCTCG
TGGACCTTCTGTCTGAAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
40 TTCCACCTTATTGGAGGGGTGGATGATTTTCTCTTTCGGTGATGGCACTTGGATCGATATG
TGGCATCTCCAAGCCCTGCACATGCGACTATCATGAGTACAGACCATTCATGATGGGCT
CACAGTGGCTGCTGGTGGGGGGCTTTGTCCACTCCATCGTGCAGATTTCCCTGTGTGCTC
CCACTCCTTTCTGCGGACCCAATGTTCTGACACTTCTACTGTGATGTCCACCGGGTCT
CAAACCTGGCCCATACAGACATTTTCACTACTGAACTACTAATGATTTCCAACAATGGACT
45 CTCACCCACACTGTGGTTTTCCTGCTCCTGGTGTCTACATAGTCATATTATTCATTACCCAA
GTCTCAGGCAGGAGGGCAGGAGGAAAGCCATCTCCACTGCACCTCCCAACATCACTGT
GGTGACCTCGCATTTCTGTCCTGCATCTATGTCTAGTCCCGGCGCTTCACTGCCCTCCCCA
TGGATAAGGCCATCTCTGTCACCTTCACTGTCACTCCCTCTGCTCAACCCCTGATCTAC
ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
TCTGATAGAAAATAG *SEQ ID NO: 306)

AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPELQALLFVTFGLGIYLLTLAWNLAFLIRGDTHLHPTMYFF
MSITFDICYSYSAVAPNMLTDFWEQKTSIFVGCQAQFFFFVGMGLSECLLLTAMAYDRYAAL
SSPLLPTMTQGLCTRMVVGAYVVGFLSSLIQASSIFRLHFCGPNINHFCDLPPVLALSCSDT
55 FLSQVNVFLVVVTVGGTSFLQLLSYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLLFGTAL

FVYLRPSSYLLGRDKVVSVFYSLVPMNLPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID NO: 307)

5 ATGTCCATAACCAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCTCTCTGGGATTCA
CAGACCATCCGAACTCCAGGCCCTCTCTTTGTGACCTTCTGGGCATCTATCTTACACC
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCATCTGCACACACCA
TGTACTTCTTCTAAGCAACTATCTTTCATTGACATCTGCTACTCTTCTGTGTGGCTCCC
AATATGCTACCTGACTTCTTCTGGGAGCAGAAGACCATATCAATTTGTGGGCTGTGCTGCT
10 AGTTTTTTTTTCTTTGTGGGATGGGTCTGTCTGAGTGCTCTCTGACTGCTATGGCATA
GACCGATATGCAGCCATCTCCAGCCCCCTTCTTACCCCACTATCATGACCCAGGGCTCT
GTACACGCATGGTGGTGGGGCATAATGTTGGTGGCTTCTGAGCTCCCTGATCCAGGCCAG
CTCCATAATTTAGGCTTCACTTTTGGGACCCCAACATCATCAACCACTTCTTCTGCGACCTC
CACCAGTCTGGCTCTGTCTTGTCTGACACCTTCTCAGTCAAGTGGTGAATTTCTCTGTG
15 GTGGTCACTGTGCGGAGGAACATCGTTCTCCAACTCCTTATCTCCTATGGTTACATAGTGT
CTCGGCTCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAGCCTGCAACACGTGTGCTC
CGCATCTGATGGTGGTGAATCTGTCTGTTGGGACAGCCCTTTCTGCTGTAACCTGGACCCAG
CTCCAGCTACTTGTAGGAGGAGCAAGGTGGTGTCTGTTTCTTATCATTTGATGATCCCC
ATGCTGAACCCCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
GTGTTGGAAGGAAGAAAGTGTTCCTTAG (SEQ ID NO: 308)

AOLFR168 sequences:

MEKINNVTIEFHWGLSPEIEKVCFVVSFFYIIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
DICYSSVTPAKMIVDILLAKDKTISYVGCMLQLLVHFFGCTEILFVVMAYDRYVAICKPLHYM
TIMNRETCKNMLLGTWVWGGFLHSIIQVALVQVLPFCGPNIDHYFCDVHPVLKLAETETVYV
25 VVVTANSGTIALGSFVILISYIILVSLRKQSAEGRRKALSTCGSHIAMVVFIFPCITFMYMRPD
TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO:
309)

30 ATGGAAAAATAAACACGTAACATGAATTCATTTTCTGGGGTCTTTCTCAGAGCCGAGAGA
TTGAGAAAGTTGTGTTTGTGGTGTCTTCTTCTACATAATCATTTCTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGGCTGAGCAACCTGTTTAACTACCCCTGATTTCTTTCTCAG
CTCTGTCTCTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCTIATGTGGGGTGCATGTTGCAACTGCTGGAGTAC
35 ATTTCTTTGGTGTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT
ATCTGTAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAAC
TACCTTTTGTGGACCAATGAGATAGATCACTACTTTTGTGATGTTACCCCTGGTTGAAA
CTTGCTGTCACAGAAACATACATTGTTGGTGTGTTGTGACAGCAACAGTGTGATCACTG
40 CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCTGATTTCCCTCGAGAAAG
CAGTCAGCAGAAAGGCGGCAAGGCCCTCTCCACTGTGGCTCCACATGCCCATGGATGCTG
TTATCTTTTTCGGGCCCTGTACTTTATGTACATGCGCCCTGATGACAGCATTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCAATTACACTCCCATGTTAAATCTCTGATTTATACAT
GAGAAATGCAGAAATGAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTCTTGGA
45 GGCTAAAGGGAATAG (SEQ ID NO: 310)

AOLFR169 sequences:

MMDNHSSATEFHLLGFGPSQGLHHILFAIFFFFYLVTLMGNTVIIIVCVCDKRLQSPMYFFLSHL
STLEILVTIIVPMLLVGLFLGCRQYLSLHVLNFCGTMETALLGVMAVDYVAVCNPLRY
NIMN SSTCIWVIVVWVWVGLSEIWPYATFQFTFRKSNLSLDFYCDRGQLKLSCDNTLLTEFI
50 LFLMAVILGSLIPTIVSYTYIISTILKIPSASGRRAKAFSTAFSGTCVVIYGSCLFLVYVKKPQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDMGRCCQLLKD (SEQ ID NO: 311)

55 ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG
GACTACACACACATCTTTTGCTATATCTTTTCTCTATTAGTGACATTAATGGGAAAC
ACGCTCATCATTTGATGTCTGTGTGGATAAACGCTGCGAGTCCCCCATGATTTCTTCTCT
CAGCCACCTCTCTACCTGGAGATCTCTGGTCAACACCAATAATGTGCCCATGATGCTTTGG

GGATTGCTCTTCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCTG
TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTATTGTGGCTGTGTGT
AACCCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTGGGTGGTAATAGTGT
CATGGGTGTTTGGGATTCTTCTGAAATCTGGCCCATCTATGCCACATTTTCAGTTTACCTTC
CGAAATCAAAATCTATAGACCATTTTACTGTGACCGAGGCAATTGCTCAAACATGTCT
5 CGGATAACACTCTTCTCAGAGTTTATCCTTTCTTAATGGCTGTTTATTTCTCATTGGT
TCTTTGATCCCTACGATTGTCTCCTACACCTACATTAATCTCCACCCTCCTCAAGATCCCGTC
AGCCTCTGGCCGGGAAGCCCTTCTCCACTTTTGCTCCCACTTCAACTGTGTTGTGATTG
GCTATGGCAGCTGCTGTTTCTCTACGTGAACCCAAACCAAGGAGTGTGATACAA
10 TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCTGAATCCTTTATCTTTACTCT
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCT
GAAAGATTAG (SEQ ID NO: 312)

AOLFR170 sequences:

15 MSFTSLPSLCSLTLPLFCYLSLLPFLSAFLFTRWLLAFLSLFSVSVPVSSVSSSMVLCLYLSVS
ASPSVFCFSCMQGPILWIMANLSQSEFVLLGFSSFGEQALYGPFLMLYLLAFMGNTHIVMVI
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLVPHKVIITFGCMVQFYHFHSLGSTSFLIL
TDMALDRFVAICHLPLRYGTILMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLIDYCHGDVINH
FFCDNEPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLSIYGYIVTTLVRIPSASSCQKAFTCG
20 SHLTLVFIYSSITFLYVRPGKAHSVQVRKVVALVTSVLTPFLNPFILTFCNQTVKTVLQGMQM
RLKGLCKAQ (SEQ ID NO: 313)

25 ATGTCTTCACTTCTCATACCCCTACTCTGTTTCTCCTTGACTCTCCCATCTCTGTTTGT
TATCTTTCTTTATTGGCCGTTTCTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCCTT
CTCTCTTATCTCTGCTCTGCTCTGCTGCTGTTTCTCTGTTTCAAGTCAATGGTCTCTGCTC
TATCTCTGTTTCTGCTCTCCGCTCTGCTCTTTGTTTCTCTTGATGCAGGGCCCCATACTG
TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCTCTTGGGCTTCTCCCTCTTGG
TGAGCTGCAGGCCCTCTGTATGGCCCTTCTCATGCTTTATCTTCTCGCCTTCATGGGAA
30 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCATGTACTTCTT
CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGACGTGCCAGGATGCTCT
CAGACCTGTTGGTCCCCCACAAGTCATTACCTTCACTGGCTGCAATGGTCCAGTCTACTCT
CAGTTTCCCTGGGGTCCACCTCTTCTCTCATCTGCAGACATGGCCCTTGTGCTGTTGT
GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGCCAGCTG
35 GCTGGGGCTGCTGGGCAGCTCCTTCTTAGCCATGGTACCCACTGTCTCTCCCGAGCTC
ATCTTGATTATCTGCCATGGCGAGCTCATCAACCACCTTCTTGTGACAAATGAACCTCTCCTG
CAGTTGTGATGCTCTGACACTCGCCTGTGGAAATCTGGGACTTTCTGATGGCCTTGACCTT
TGTCTCTCAGCTCCTTCTGGTGACCTCATCTCCTATGGCTACATAGTGACCACTGTGTGTC
GGATCCCTCTGCCAGCAGCTGCCAGAAGGCTTCTCCACTTGGCGGTCTCACTTCACT
40 GTGCTTCACTCGGTACAGTAGTACCATCTTCTGTATGTGAGGCTGGCAAGTCACTCT
GTGCAAGTCAGGAAGGCTGTGGCCTTGGTGACTTCACTTCACTCCCTTCTCAATCCCT
TTATCTTACCTTCTGCAATCAGACGTTAAACAGTGCTACAGGGGCAGATGCAGAGGCT
GAAAGGCTTCTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

45 MVGNLLIWTITGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLLCDKIAISLSACMGQLFI
EHLNGGAEVFFLLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVMAMIGGFVHSVVQIVFLYSLP
ICGNPNVIDHSVCDMPYLLLELLCLDTYFGLTVVANGGHCMVIFTLLISCGVILNFLKTSQEER
HKALPTCISHIIVVALVFVPCIFMYVRPVSNFFPDKLMTVFYSIITLMLNPLIYSLRQSEMKNAM
KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

50 ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCTCCTTGGGCTCCCTAA
TGTACTTCTCTCTGCTACTTGTCACTTATGGATGGCATATATCCACTGCCATGTACACC
AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTCTCTGTGACGTTGATGGGTG
AGCTCTTCATAGAACACTTACTTGGTGGTGCAGAGGTCTTCTCTTGGTGGTGTGAGGCTA
55 TGATCGCTATGGGCTATCTCTAAAGCCGCTGCACTATTGAACCATCATGAATCGACTGGT
TGATCCTTCTGTTGGTGGTGCCATGATTGGAGGTTTGTGCACTCTGTGGTTCAAATTGT

CTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
 ACCCATTTGTTGGAACCTGTTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
 TGGTGGGAATAATTTGTATGGTCACTCTTACCTTTCTGCTAATCTCCTGTGGAGTCAATCCTAA
 ACTTCCCTTAAAACTTACAGTCAGGAAGAGAGGGCATAAAGCCCTGCCTACCTGCATCTCCCA
 CATCATTTGGTTGGTTCGCCCTCGTTTTGTTCCTCTGATTTTATGTATAGACCCGTTTCCA
 ACTTTCCCTTTGATAAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTGGAATCCT
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGGTGA
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCCACTGAACATATTTATTCTAGTCTCA
 AGGCAACAATAGGCGGTAA (SEQ ID NO: 316)

AOLFR172 sequences:

MAETLQNSITFLHPNFFILTFGPGLGSAQTLWTLVFGPIYLALLNGALPAVVWIDSTLHQP
 MFLLLAILAATDLGLATSIAPGLLAVLWLGPRSVFYAVCLVQMFVHALTAMESGVLLAMACDR
 AAAIGRPLHYVVLVTKACVGYAALALALKAIVAVVPPFLLVAKFEHFQAKTIGHTYCAHMAV
 VELVVGCTQATNLGYLGLALSIAISGMDILGITGSYGLIAHAVLQLPTRAHAKAFGTCSSHICVIL
 AFYIPGLFSYLAHRFHHTVPKPVHILLSNIYLLPPLNPLIYGARTKQIRDRLETTFFRKSPL
 (SEQ ID NO: 317)

ATGGCAGAAACTCTACAACCTCAATTCACCTTCTACACCCAACTTCTTCATACTGACTG
 GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGCACCTGGCTTTTGGGCCAATTTATCT
 GCTGGCCCTGCTGGGCAATGGAGCACTGCGGGCAGTGGTGTGGATAGACTTCCACCTGCA
 CAGGCCATGTTTCTACTGTTGGCCATCTGGCAGCCACAGACCTGGGCTTAGGCCACATCT
 ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCGCATCTGTGCCATATGCTGTGT
 GCTGTGTCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
 CATGGCTGTGATGCTGCGGCAATAGGGCGTCCACTGCACCTACCCTGCTCGGTGCCACC
 AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
 CTTTCCCACCTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAAGACCATAGGCCATACCTA
 TTGTGCACACATGGCACTGGTGAAGAACTGGTGGTGGGTAACACACAGGCCAACCACTATA
 TGGTCTGGCACTTTCAGTGCCATCTCAGGTATGGATATTCTGGGTATCATGCTGGCTCAT
 GGACTCATTTGCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCCTTGT
 GTACATGTAGTTCTCACATCTGTGTCTTCTGGCCTTCTACATACCTGGTCTCTCTCCTAC
 CTCGACACCCGCTTTGGTCTACACACTGTCCAAAGCCCTGTGCACATCTCTCTCCAAAT
 CTACTGTCTGTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAGCAGATC
 AGAGACCGACTCCTGGAAACCTTCAACATTCAGAAAAAGCCGTTGTAA (SEQ ID NO: 318)

AOLFR173 sequences:

MSHTNVTIFHPAVFVLPGIPGLEAYHIWLSIPLCLJIYITAVLNSILIVVIMERNLHVPMYFFLS
 MLAVMDILLSITTVPKALAIWQLAHNIAFDACVTQGGFVHMMFVGESAILLAMAEDRFVAIC
 APLRYTTLVTPVVGRIALAVITRSFCHIFVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
 NIWYGSVPWPMVILDVILIAVSYSLILRAVFLPSQDARHKALSTGSHLCVILMFYVPSFTLL
 THHFGRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREGVAHRFFDIKTWCCTSPLGS
 (SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCTGCACTTTTGTCTTCTGCGCATCCCTGG
 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTGGCTCATTTACATCACTGCAGTCC
 TGGGAAACAGCATCCTGATAGTGGTTATTGTCATGGAAAGTAAACCTTCTATGTGCCATGTA
 TTTCTTCTCTCAATGCTGGCCGTCATGGACATCTGCTGTCTACCACTCATGTGCCAAAGG
 CCTAGCCATCTTTGGCTTCAAGCACATAAATCTGCTTTTGTAGCTGTCTACCAAGGCTTGT
 TCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGTCAACATGGCCTGTTGTGGG
 AGGATTGCTCTGGCCGTCATACCCGAAGCTTCTGCATCATCTTCCAGTCATATTTCTGTCT
 GAAGCGGCTGCCCTCTGCTTAACCAACATTGTTCTCTCACTCTCATGTGAGCATATTGGA
 GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTTGGTATGGCTTCTCAGTGCCAT
 TGTCTATGGTCACTTGGATGTTATCTCTCATCGCTGTGTCTTACTCACTGATCTCCGAGCAG
 TGTTTCTGTTGCCCTCCAGGATGCTCGGCACAAAGGCCCTCAGCACTTGTGGCTCCACCT
 CTGTGTCATCTTATGTTTATGTTCCATCTCTTTTACCTTATTGACCATCATTTTGGGGG

TAATATTCTCAACATGTCCATATCTTGCTGGCCAATCTTTATGTGGCAGTGCCACCAATGC
TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCGGTT
CTTTGACATCAAGACTTGGTGCTGTACCTCCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

5 **AOLFR175 sequences:**

MHFLSQNDLNNLIPHLCLHRHSVIAGAFTHRHMKIFNSPNSSTFTGFILLGFPCPREGQILLFV
LFTVVYLLTLMGNSGIIICAVHWDQRLHAPMYILLANFSLEICYVTSTVPMSMLANFLSDTKIISF
SGCFLQFYFFSLSGSTRCEFFLAVMAFDRLYLACRPLRYPTIMTRRLCTNLVNCWVLGFIWFLPI
VNISQMSFCGRJIIDHFLCDPAPLLTLCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVVRVAVL
10 RVPAAAGRRKAFSTCGSHLAVVSLFYGSVLVYMGSPSPKNEAGKQKTVTLFYSVVTPLNPNVI
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAAATGATTTAAATATAAACTCTGATTCCTCCATCTATGTTTGACCG
15 TCATTAGTAATTTGCTGGTGCTTTTACAATTCACAGGCACATGAAAACTTCAACAGCCCC
AGCAACTCCAGCACCTTCACTGGCTTCACTCCTCTGGGCTTCCTTGCCTCCAGGAGGGGC
AGATCCTCCTCTTTGTGCTTCACTGTTGTTACCTCTGACCCCTATGGGCAATGGTTCC
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCAGCCCCCATGTACATCCTGCTCGCCA
ACTTCTCCTTCTTGAAGATATGTTATGTCACTCCACAGTCCCCAGATGCTGGGCAACTTC
20 CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTCTCCCTCCAGTCTACTTTTCTTCTCC
TGTGGCTCTACGAATGCTTTTCTGCGCAGTTATGGCATTGTATCGTACCTTGTCCATCTG
TCGGCTCTACGCTATCCAAACCAATTATGACACAGCTCTCTGTACCAATCTTGTGGTCAAT
GCTGGGTACTTGGTTTCACTCTGGTTCTTGATTCTCTATCGTCAACATCTCCCAAAATGCTCTTC
TGTGGATCTAGGATTATGACCACTTCTATGTGACCCAGCTCCTCTCTCACTCACTCACTTG
25 CAAAAAGGCCCTGTGATAGAGCTTGTCTTTCTGTCTTAAGTCTCTGCGCTGCTTTAIGC
TCTTTCTCTTCAATTGTGGGGTCTATGCTCTGGTCTGAGAGCTGTGTTGAGGGTCCCTTCA
GCAGCTGGGAGAAAGAAAGGCTTCTCCACCTGTGGGTCTCACTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCACTGTATGGGAGCCCACTCTAAGAATGAAGCTGGAAGAGC
AGAAGACTGTGACTCTGTTTATCTGTGTTGTTACCCCACTGCTTAACCTGTGATATATAGT
30 CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTTGGGGAACATA (SEQ ID NO:
322)

AOLFR176 sequences:

MFFIIHSLVTSVFLTAGPQNRTMHFVTEFVLLGFHGQREMQSCFFSFLVLYLLTLLNGAIVC
35 AVKLDRLRLHTPMYILLGNFALEIWIYSTVPMNMLVNILSEIKTISFSGCFQFYFFSFLGITECF
LSVMAYDRLYLACRPLHYPYSIMTGKFCILVCVCWVGGLFCYPVPIVLISQLPFCGPNIIDHLVCD
PGPLFALACISAPSTELICYTFNSMIHFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSTPSGNPAGMQKIITLVYATMPFLNPLIYSLRNKDMKDLKRVLGLTVS
QN (SEQ ID NO: 323)

40 ATGTCTTTIATTATTCATTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA
CAGCAACATGCATTTTGTGACTGAGTTTGTCTCTCGGGTTCCATGGGTCAAAGGAGATG
CAGAGCTGCTTCTTCAATTCATCTCGTTTCTCTATCTCTGACACTGCTAGGGAATGGAGC
TATTGTTCTGTGCAAGTGAATTTGGACAGGCGGCTCCACACCCATGTACATCTCTCTGGGA
AACTTTCCTTTCTAGAGATCTGTGATATTTCTCCACTGTCCCAACATGCTAGTCAATAT
45 CCTCTCTGAGATTAACCACTCTCCTTCTCTGTTTGTCTCTGCAATTCATTTCTTTTCTC
ACTGGGTACAACAGAGTGTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTGCTGCAATACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAAATTTCTGGTCTGTGT
ATGTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTCTCT
TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCATTGTTTGACATGGC
50 CTGATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCTACAGAGCTGTGCTTTGATTCCT
TCTGGTCTGTGTCGAACATAAGCTTCTCCACATGTGGGTCCCACTAATGGTGGGTGTCT
TATTCTATGGAACCTTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTTCTTAATCCCTTATCTAT
55 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTGGGGTTAACAGTTAGC
CAAACTGA (SEQ ID NO: 324)

090505Z 062001

5

10

15

20

25

30

30

35

40

45

50

55

55

ATGAATGGAATGAATCACTCTGTGGTATCAGAAATTTGTATTCATGGGACTACCAACTCAC
 5 GGGAGATTACAGCTTCTACTTTTGTTTTCTCTTTGTGTCTACTTTGCGAGCATGATGGGA
 AACCTTGTTCATTGTATTCATGTAACCATGGATGCTCATCTGCACCTCCCCCATGTATTTCTC
 CCTGGCTAACCTCTCAATCATTTGATATGGCAATTTGCTCAATTACAGCCCCAAGATGATTT
 GTGATATTTTCAAGAAGCACAAAGGCCATCTCCTTTCGGGGATGTATTACTCAGATCTTCTT
 TAGCCATGCTCTTGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC
 ATGGCCATATGATAAACCCTTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT
 10 TTTTAGCCACTTCTCTATCATTTGGCCTTATCCACTCATTTGGTCCAAATAGTTTTTGTGGTA
 GTTTTACCTTTTGTGGGTCTAATAATCTTTGACAGTTTTACTGTGATCTCCCTCGGCTCT
 CAGACTTGCCCTGTACCAACACCCAGAAGCTGGAGTTCATGTGCATGTCAATAGTGGAACT
 ATTTCTGTGGGCTCCTTTGTCTTGGTGGTAATTTCCACATCTTCATCTGTCTCACTGTTTG
 GAAACATCTCTCTGGTGGTCTAGCCAAGGCCCTCTACCTGTCACTCATGTCACTGTG
 15 GTCATCTTGTCTTTGGGCCACTGATGTTTTCTACACATGGCCTTCTCCACATCACACCT
 GGATAAATATCTGCTATTTTTGATGCAATTATTACTCCTTTCTGAATCCAGTTATCTACA
 CATTACAGGAACAAAGACATGAAAGTGCCAATGAGGAGACTGTGCAGTCGCTTTCGCCATT
 TTACAAAGATTTTGTA (SEQ ID NO: 330)

AOLFR180 sequences:

20 MTNKMVIAIYKLNLYFSEFLIVQCLQPTMAIFNNTTSSSNFLTAPFGLECAHVWISIPVCCLYTI
 ALLGNSMIFLVIITKRLHLKPMYYFLSMLAAVDLCLTITLPTVLGVLFWHAREISFKACFIQMF
 FVHAFSLLESSVLPAMAFDRFVAICNPLNYATILDRMVLVIGLVICIRPAVFLPLLVAINTVSF
 HGGHELSPHCYHVEVIKYITYSKPWISSFWGLFLQLYLVNGTDVLFILFSYVLIRVTLGVARKK
 QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSFTRVLCSTLANIYLLPPVLNPHIYSLKTKTR
 25 QAMFQLLQSKSGWGFNVRLGRWRD (SEQ ID NO: 331)

ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTCTTTCCTCATAGT
 TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACCACTTCGCTCTTCCTCAAACTTCC
 30 TCCTCATGCAATCCCTGGGCTGGAATGTGCTCATGCTGGATCTCCATCCAGTCTCGTGT
 CTCTACACCAATTGCCCTTTGGGAAACAGATGATCTTTCTTGTCATCTTACTCAAGCGGA
 GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
 ATTACGACCCCTCCCACTGTGCTTGGTGTCTCTGGTTTCATGCCCGGAGATCAGCTTTAA
 AGCTTGTCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGGTGAGTCCCTCGGTGCTGG
 TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCACTGAACTATGCTACTATCCTC
 35 ACAGACAGGATGGTCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTTCTTAC
 TTCCCTTCTTTGAGCCATAAACAAGTGTCTTTTCAATGGGGGTACGAGCTTTCCCATCCA
 TTTTGTACCAACCCAGAAGTGATCAAATACACATATCCAAACCTTGGATCAGCAGTTTTT
 GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATCTTTTCTCCTAT
 40 GTCTGTATCTCCGTACTGTCTCTGGGCATTTGTGGCCGAAGAAGCAACAAAAGCTCTCA
 GCATCTTGTCTGTCTGACACTGTGCACTGCTATTTCTATGTGGCACTGACGCTCTCT
 TTGGCACACCGCTCTTCCACTCCACCCCAAGGGTGCTGTGAGCACTTTGGCCAATATTATTA
 TCTGCTCTTACCACTGTGCTGAACCTCATTTACAGCTTGAAGACCAAGCAATCCCGC
 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTTAATGTGAGGGGTCTTA
 45 GGGGAAGATGGGATTGA (SEQ ID NO: 332)

AOLFR181 sequences:

MSVLLNNEVLFLLIGIPGLEHAHWFSPICLMYLLAIMGNCTILFIKTEPSLHEPMMYYFLAML
 AVSDMGLSSLPMTLVRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNP
 50 YSSILTSNRVAKMGLILAIRSILLVIPFPFTRRLKYCQKNLLSHSYCLHQDTHKLCASDNKTNV
 IYGFIIALCTMDLALIVLSYVILKLTILSIASLAERLKAALNTCVSHICAVLTFYVPHITLAAMHHF
 AKHKSPVLVILIADMFLVPPLMNPIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTCTCTGATTGGGATCCCAGGACTGG
 AACATGCCACATTTGGTTTCCATCCCCATTTGGCTCATGTACCTGCTTGGCATCATGGGG
 55 AACTGCACCATTTCTCTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATT
 CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCCATACCATGTGA

GGGTCTTCTTGTTCATGCCATGGGAATTCACCTAATGCCTGCTTTGCTCAAGAATCTTCT
ATTCATGGATTCACTGTGCATCGGAATCTCCAGTACTTCTAATTATGCTTTGGGACCGTTTCT
TGCCATTCACAATCCCTTAAGATACAGTTCTATCTCTACTAGCAACAGGGTTGCTAAAATG
5 GGACTTATTTAGCCATTAGGAGCATCTCTTAGTGATTCCATTCCCTTCACTTAAGGAG
ATTAAAAATTGTGTAAGAAATCTCTTTCTCACTCATAGTCTCTCATCAGGATACCATGA
AGCTCGCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCAITGCTCTCTGTACT
ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGCTCCACATCTGTGCTGTG
10 CTCACCTTCTATGTGCCATCATCACCCTGGCTGCCATGCATCACTTTGCCAAGCACA
GCCCTCTTGTGTGATCTTATTTGAGATATGTTCTTGTGGTGCCGCCCTTATGAACCC
ATTGTGTACTGTGTAAGACTCGACAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

- 15 MTLGSLGNSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVISIPGNTCLIFIKTSLHEPMYFL
SMLALIDLGLSLCTLPTVLGIFVWVGAREISHDACFAQLFIHCFSESSVLLSMADRFVAICH
LHYVSLTNTVIGRIGLVSLGRSVAILFPLPMLKRFPYCGSPVLSHSYCLHQEVMLACAMK
ANSIYGMFVIVSTGIDSLILFSYALIRTVLSIASRAERFALNTCVSHICAVLLFYTPMIGLSV
IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVYSVKTKQIRDRVTHAFY (SEQ ID NO: 335)
- 20 ATGACCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCTGCTGAGTG
GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT
GGTTTCCATCCCGGCAACTGCACAATCTTTTATCATTAACACAGCGCTCACTTCAT
25 GAACCTATGATATCTTCTCTGTCATGCTGGCTCTGATTGACCTGGGTCTCCCTTTGAC
TCTCCCTACAGCTCTGGGCATCTTTGGGTGGAGCAGAGAAATTAGCCATGATGCTGCTG
TTTGCTCAGCTCTTTTCACTACTGCTTCTCTTCTCGAGTCTCTGTGCTACTGTCTATG
GCCTTTGACCGCTTTGTGGCTATCTGCCACCCTTGCACTATGTTTCCATCTCACCAACAC
AGTCATTTGGCAGGATTGGCCTGGTCTCTCTGGGTCGTAGTGAGCACTATTTTCCATTA
30 CCTTTATGCTCAAAAGATTCCCTATTGTGGCTCCCCAGTTCTCTCATCTTCTATGTGCT
CCACAAGAAAGTGATGAAATGGCCTGTGCCGACATGAAGGCCAACAGCATACCGGCTG
GTTTGTCTCGTCTACAGTGGGTATAGACTCACTGCTCATCTCTTCTTATGCTCTGA
TCCTGCCACCGTGTCTCCATCGCCTCCAGGCTGAGAGATTCAAGGCCCTAACACCTG
TGTTTCCACATCTGTGCTGTGCTGCTCTTACACTCCCATGATTGGCCTCTCTGTCATCC
ATCGCTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTCAAGGTTCACTGATATCTTCT
35 CTTTCTCTGTGATGAATCCCATTTGTCTACAGTGTGAAGACCAACAGATCCGGGATCGA
GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

AOLFR183 sequences:

- 40 MTNLNASQANHRNFILTGIPGTPDKNPWLAFLGLFYTLTLLGNGTILAVIKVEPSLHEPTYFL
SILALTDVSLMSLTPLSMLSIYWFNAPQIVFDACIMQFFHVFIVESGVLSVMAFDRFVAIRN
PLHYVSILTHDVIRKTGISVLTRAVCVVFPVFLIKCLPFCHSNVLSHSYCLHQNMRLACASTR
INSLYGLIVIFLGLDVLTLTLLSYVLTLKTVLGIYSRGERLKTSLCSLHMSITLVIFYVPMGA
ASMIHRWFHFLSPVHVMADIYLLPPVLNPVYSVKTKQI (SEQ ID NO: 337)
- 45 ATGACGAACCTGAATGCATCACAGGCCAACCCGTAACCTTCTTCTGACAGGTATCCCA
GACGCCAGACAGAACCCATGGTTGGCCTTTCCCTGGGATTTCTCTACACACTCACACT
CCTGGGAAATGGTACCCTCCTAGCTGTGCATCAAGGTGGAGGCCAGTCTCCATGAGCCCTCAG
TATTACTTCTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCATGTCCACTTGCCTTCC
50 ATGCTCAGCATCTACTGTTTAAATGCCCTCAGATTGTTTGTGATGCATGCATCATGCAGAT
GTTCTTCACTGATATTGGAAATAGTAGAATCAGGAGTCTAGTGTCCATGGCCTTTGAC
AAGATTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTACGATGTTATTGC
AAGAGCTGGAATATCTGCTCCTACCCGGGAGCTGTGTGGTATTCCTGTGCCCTTCCT
ATAAAGTGCCTACCTCTGCTGCTTCCCATTCATCTTCACTACTGTCTTACCAAAAA
CATGATGGCGGTAGCTGTGTCAGCACCCTGATCAACAGCCTTACGGCCTCATGTGCTG
55 ATCTTCACTAGGCGCTGATGTTCTCTCACTCTACTGTCTTATGACTACCTTGAAGAC
TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAACCCCTACGACATGCCTCTCTCAC

ATGTCTACCGTGCTCCTCTTCTATGTTCCCTTTATGGGTGCTGCCTCCATGATCCACAGATT
TTGGGAGCATTATACCCAGTAGTGCACATGGTCATGGCTGATATATACCTACTGCTCCCC
CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

5 **AOLFR184 sequences:**

MS1LPTQIAPNSSTSMAPTFLLVGMPLSGAPSWWTLPLIAVYLLSALNGTILWIALQPALHR
PMHFFLLSVSDIGLVTALMPTLLGIALAGAHVTPASACLLQMVFHFVSVMESSVLLAMSID
RALAICRPLHYPALLTNGVISKSLAISFRCLGLHLPLPFLLAYMPYCLPQVLTSHSYCLHPDVARI
ACPEAWGAAYSFLVVLSAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLASVLLF
10 YIPMILLALINHPLEPITQHTHTLLSYVHFLPLINPILYSVKMKEIRKRLNLRQPRKVGAQ
(SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCACCTTCT
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCTCTGGTGGACATTGCCCTCATTGC
15 TGCTACCTTCTCTCTGCACCTGGGAAATGGCACCATCTCTGGATCATTGCCCTGCAGCCC
GCCCTGCACCGCCCAATGCACCTTCTTCTCTCTTCTGCTAGTGTGCTGATATTGGATTGGT
CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTTGCTGGTGTCTACACTGTCCTCGCC
TCAGCTGCCCTCTCAGATGGTTTTATCCATGCTCTTTCTGTCATGGAGTCTCTCGTCT
20 GCTGCCATGTCCATTGATCGGGCACGGCCATCTGCCACCTCTCCACTACCCAGCGCTC
CTACCAAAATGGTGTAATTAGCAAAAATCAGCTGGCCATTTCTTTTCGATGCTCGGCTCTCC
ATTGCCCTGCCATTCTGCTGGCCTACATGCCCTACTGCCCTCCACAGGTCTCAAAACCAT
TCTTATTGCTTGATCCAGATGTGGCTCGTTTGGCCTGCCACAGAAGCTTGGGTGTCAGCCT
ACAGCCTATTGTGGTTCTTTCAGCCATGGGTTTGGACCCCTGCTTATTCTTCTCTCTAT
25 GGCCTATTGGTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGGAGTCCGTGGAAAGGCTGGT
CAAACTGTGCTGCCACCTCTCTGCAGTGCTCCTCTCTATATCCCTATGATCTCTCGGC
ACTGATTAACCATCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCTCTATGTCC
ATTTCCTTCTCTCCATTGATAAACCTTATCTCTATAGTGTCAAGATGAAGGAGATTAGA
AAGAGAATACTCAACAGGTTCGACCCAGGAAGGTGGGTGTGCTCAAGTA (SEQ ID NO:
340)

30

AOLFR185 sequences:

MFYPILNDISTKNNNSIMSCCNILFIKTVEIILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR
VDCVPSRDHINQSMVLASGNSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR
IDHTLHEPMYLFLAMLAITDLVSSSTQPKMLAIFWFHAEIQYHACLQVFFHAFSSVESGVL
35 MAMALDCYVATCFPLRHSSILTPSVVIKLGTHVMLRGLLWVSPPCFMVSVMRMPFQHQKAFPSYC
EHMAVLKLVCADTSSIRGYLGFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
SHVICLALYNPALFSFLTYRGHDVPRVVHILFANLYLLPIMPNLPHYGVRTKIQGDRVIQGGCG
NIP (SEQ ID NO: 341)

40 ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTGATGTT
GTAAACATATTATTATAAAAACAGTTGAAATATTCTAGTTTATAATCAAAACCAATCACCC
CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAAACACTTGTTTGTAGTTGT
ATCATCTGCAGAGATAGATTGCGTTCACGACGAGACCATATTAACCAAGTCCATGGTGCT
45 GGCCTCAGGGAACAGCTCTTCTCATCTCTGTGCTCTCATCTCGTGTGAATGCCAGGCCTG
GAGAGTTTCCAGTTGTGGATTGCCTTCCGTTCTGTGCCACGATGCTGAGTGGCTGTGTGG
AAATCACTCTCTCCATGTAATCAGAATTGACCACACCTGCAATGAGCCCATGTACCTC
TTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCTCTCCACTCAACCTAAGATGTT
GGCCATATTCTGGTTTCATGCTCATGAGATTCACTACCATGCTCGCTCATCCAGGTGTTCT
TGATCCATGCTCTTTTCTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACGTGCTAC
50 TGGGCTACCTGCTTCCCACTCCGACACTAGCATCTGACACCCCATCGGCTGATCAAAAC
TGGGACCAATCGTGAAGTCTGAGAGGGCTGCTGTGGGTGAGCCCTCTGCTTTCATGGTGTC
TAGGATGGCCTTCTGCCAACCAAGCCATTCCCCAGTCATACTGAGCAACATGGCTGTG
CTGAAGTTGGTGTGCTGATACAAGCATAAAGTCGTGGGTATGGGCTCTTTGTGGCCCTT
CTGTGGCTGGCTTTGATGATGTTGTCATTGGTATGTCATACGTGATGATTTGAGAGCTGT
55 GCTTCAGTTGCCCTCAGGTGAAGCCCGCCTCAAAGCTTTTAGCACACGTGCCCTCCCATATC
TGTGTCATCTTGGCTCTTATATCCAGCCCTTTTCTTCTCTCACTACCGCTTTGGCCAT

098505.062201

1030-1039

5

10

15

20

25

30

35

40

50

55

AOLFR190 sequences:

5 MQRSNHVTETILLGFTTDPGMQLGLFVVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
LSFLDLWYSSVHTPKILVTCISEDKSFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
YAQTMPRRLCICLVLYSYTGGFVNAIILTSNTFTLDPCGDNVIDDFCDVPLVKLACSVRESYQ
AVLHFLASNVISPTVLILASYSIHITLRIHSTQGRKVFSTCSSHLISVTLYYGSLYNYSRPSSS
YSLKRDKMVSTFTYMLFPMLNPMIYSLRSKMDKALKKFFKSA (SEQ ID NO: 351)

10 ATGCAGAGGAGCAATCACACAGTGACTGAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
GGATGCAACTGGGCCCTTTGTGGTGTTCCTGGGTGTGTAAGTGTGCTGACTGTGGTAGGAAG
TAGCACCCCTCATCGTGTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTGTCA
TTGGAAATCTGTCATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG
ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCGCTGTGTCAGTTCTCTCTGC
CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
ATCTCCAAGCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTT

15 ATATTCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTACATTG
GATTTTTGTGGTGACAATGTCAATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCTTCTGGCCTCCAATGTC
ATCTCCCTACTGTGCTCATCCTTGCCCTCTTACCTCTCCATCATCACCAACCATCCTGAGGAT
CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCACCTGATCTCCGTTA

20 CCTTATACTATGGCTCCATTCTCTACAACACTCTCCGGCCAAATTCCAGCTACTCCCTCAAG
AGGGACAAAAATGGTTTCTACCTTTTATACTATGCTGTTCCTCATGTTGAATCCCATGATCTA
CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATCTTCAAGTCAGCATAA
(SEQ ID NO: 352)

AOLFR191 sequences:

MTDGGNITEITYFILLGFSDFPRIJKVLFTIFLVITYTSLAWNLSLIVLRMDSHLHTPMYFFLSNLS
FDVCYISSTVPKMLSNLLQEQQTTTFVGCIIQYFIISTMGLSECLMTAMAYDRYAACNPLLYS
SIMSPTLCVMMVLGAAYMTGLTASLFGIALLQLHFHCGSNVIRHFFCDMPQLLILSCTDITFFVQV
5 MTAITLTMFFGIASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSGIFVYLRSSS
GGSSSDFRFAVSFVYVIPMLNPLIYSLRNKEIKDALRKLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCAGATT
10 TCCCAGGATCATAAAGTGCTCTTCACTATAATCCTGGTGATCTACATTACATCTCTGGCC
TGGAACCTCTCCCTCATTTGTTTAAATAAGGATGGATTCCCACTCCATACACCATGTATTT
CTTCTCTCAGTAACCTGTCTCTCATAGATGTCTGCTATATCAGCTCCACAGTCCCAAGATGC
TCTCCAACTCTTACAGGAACAGCAAACTATCACTTTTGTGGTGTGATTATTCAGTACTTT
ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
15 ATGCTGCCATTTGTAAACCCCTGCTCTATTATCATCCATCATGTCAACCCACCTCTGTGTTTGG
ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATCCAAATTGGTGCTTTGCT
TCAACTCCACTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCAACTGT
TAATCTTGTCTGTACTGACACTTCTTGTGACAGGTCATGACTGCTATATTAACCATGTTC
20 TTGGGATAGCAAGTGCCCTAGTTATCATGATATCTCATGGCTATATTGGCATCTCCATCA
TGAAGATCATCTCAGCTAAAGGCAGTCCAAAGGCATCAACACCTGTGGCTTCTCATTAAC
AGCTGTTTCCCTCTTCTATACATCAGGAATCTTGTCTATTTGAGGTCAGCTGTGGAGTT
CTTCAAGCTTTGACAGATTGTCATCTGTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
TTGATTACGATTTGAGGAACAAAGAAATTAAGATGCCTTAAAGAGGTGCAAAAGAGA
AAGTGCTGCTGA (SEQ ID NO: 354)

AOLFR192 sequences:

MENNTEVTEFIVLGLTDDPELQIPLFIVFLFIYLLITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
DFGYSSAVTPKVMVGLTGDKFILYNACATQFFFFVAFITAESFLLASMAFYDRYAALCKPLHY
TTTMTTIVNCALAGSYICGFLNASIHTGNTRFLSFCRSNVVEHFFCDAPPLLTLCSDNYISEM
VIFVVVGNDLFSILVILISYLFIFITIMKMRSPGKQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
30 HFMTGDKMASVFFYAVIPMLNPLVYSLRNKEVKSFAFKKTGVKAKASGIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTATCCTTGTGGGGTTAACTGATGACCCAGAA
CTGCAGATCCCCTCTTCATAGTCTTCCCTTTCATCTACCTCATCACTCTGGTTGGGAACCT
GGGGATGATTGAATTGATTCTACTGGACTCTGTCTCCACACCCCCATGACTCTTCTCTCA
35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
GTTTCTCAGCAGGACAAATTATATTAATAATGCTTGTGCCACACAATTTCTCTCTTGTG
TAGCCCTTATCACTCAGAAAGTTTCTCTGGCATCAATGGCCTATGACCGCTATGCAGC
ATTGTGTAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTGTGCTGGCC
40 ATAGGCTCTACATCTGTGGTTTCTGAAATGCATCCATTATCATCTGGGAACACTTTCAGGC
TCTCCTTCTGTAGATCCCAATGTAGTTGAACACTTTTCTGTGATGCTCCTCCTCTCTTGACT
CTCTCATGTTTCAGACAACATACATCAGTGAGATGGTTATTTTGTGGTGGGATTCATG
ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATTTATCACCATCATGAAG
ATGCGCTCAGCTTGAAGGACGCCAGAGGCCCTTTCTACTTGTGCTTCCCACCTTACTGCAG
45 TTTCATCTTTATGGGACAGGAATCTTTATGTACTACGACCTAATCCAGCCATTTTCATG
GGCAGACAAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
TCTACAGCTGAGGAACAAAGAGGTAAAGATGCCTTTAAAAAGACTGTAGGGAAGGCA
AGGCCTCATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

MENKTEVTQFILLGLTNDSELQVPLFTTFPIYITLVGNLGIIVLIFWDSCLHNPMYFFLSNLSLV
DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMAFYDRYAACVCKPLHY
TTTMTTIVCARLAGSYICGFLNASIHTGDTFSLSPCKSNEVHHFFCDIPAYMVLSCSDRHISEL
VLIVVVSFNIFIALVILISYTFIFITLKMHSASVYQKPLSTCASHFIAVGIFGTIIFMYLQPSSSH
SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSFAFKKVVEKAKLSVGWSV (SEQ ID NO:
55 357)

ATGGAATAAGACAGAAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
 CTGCAGGTTCCCTCTTTATAACGTTCCCTTCATCTATATTATCACTCTGGTGGAAACCT
 GGGAAATTATGTAATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTCTCA
 GTAACTTGCTCTAGTGGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA
 5 TTCTTATAGAAGACAAGGTCACTCTTACAATGCATGTGCTGCTCAAAATGTATATCTTGT
 AGCTTTTGCCACTGTGGAAAATTACCTCTGGGCTCAATGGGCTATGACCGCTAGCAGCA
 GTGTGCAAAACCTACATTACACCACAACCATGACAACTGTGTGTCTGTCTGGCCA
 TAGGCTCTCACTCTGTGGTTTCTGGAATGCCTCCATCCCACTGGGGAGCAATTTAGTCTC
 TCTTTCTGTAAGTCCAATGAAAGTCCATCACTTTTCTGTGATATTCAGCAGTCATGGTTCT
 10 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTTCTTATTTAGTTGTGAGCTTCAATATCT
 TTATAGCTCTCTGGTATCTTGATATCTACACATTCACTTTTATCACCATCTCAAGATCG
 CACTGAGTTCAGTATACCAAGAAGCTTTGTCCACTGTGCTCTCACTTCAATTCAGTCGCG
 CATCTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACITCCATGGACA
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCCTGGTCTA
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

MERQNSQCVVEFILLGFSNYPELQGQLFVAFVLVIYLVTLIGNAIIHIVVSLDQSLHVPMYLFLNL
 20 SVVDLSFSAVIMPEMLVVLSTETKTSIFGGCAQMYFILLFGGAECFLGLGAMAYDRFAICHPL
 NYQMIMNKGVMFKLIIFSWALGFMLGTVQTSWVSWSPFCGLNEINHISCTPAVLELACADTLF
 FEIYFTGTFLIILVFFLLILLSYRVLFAILKMPSTTGRQKAFSTCAHLTVSVTLFVGTSMTYLQ
 PKSGYSPETKKVMSLSYLLTPLNLLIYSLRNSEMKRALMKLWRRRVVLTHT (SEQ ID NO:
 359)

ATGGAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
 CTGAGCTCCAGGGGACGCTCTTTGTGGCTTCTCTGGTTATTTATCTGGTGACCCCTGATAGG
 AAATGCCATTTATATGATCATCGTCTCCCTAGACAGAGCCCTCCAGTTCCTATGACCTGT
 30 TTCTCTCGAACTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTATTTATGCTTGAATGCT
 GGTGGTCTCTCTACTGAAAAAACTACAATTTCTTTGGGGGCTGTTTGCACAGATGTAT
 TTATCTCTTTTGTGGTGGGGCTGAATGTTTCTCTGGGAGCAATGGCTTATGACCGATT
 TGCTGCAATTTGCCATCTCTCAACTACCAAAATGATTGAAATAAAGGAGTTTATGAAA
 TAAATATATATTTCAATGGGCTTAGGTTTATGTTAGGTACTGTTCAAAACATCATGGGTATC
 35 TAGTTTTCCCTTTGTGGCCTTAATGAAATTAACCATATATCTGTGTAACCCAGCAGTGT
 TAGAACTTGCATGTGCAGACACGTTTTTGTGTAATCTATGCATTCACAGGCACCTTTTGT
 ATATTTTGGTTCCTTTCTGTGTGATCTCTGTCTTACATTCGAGTCTGTTTGGCCATCTG
 AAGATGCCATCAACCACTGGGAGACAAAAGGCGTTTCCACCTGTGCCGCTACCATCATC
 CTGTGACCCATATCTATGGCACGCCAGTATGACTTATTTACAACCCAAATCTGGGTACTC
 40 ACCGGAACCAAGGAAAGTGAATGATGTCATTGTCTTACTCACTCTGACACCACTGCTGAATCTG
 CTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATATGCGGAAGG
 CGAGTGGTTTTACACAACTCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

MIVQLICTVFLAVNTFHVRSFDFLKADDMEINQTLVSEFLLGLSGYPKIEIVYFALILVMY
 45 LVILIGNVLIASFDFSHFTPMYFFLGNLSFLDICYSSVPSLTVLSLKKRNISFSGCAVQMFF
 GFAMGSTCELLGMMAFDRYVAICNPLRYPIILSKVAYVLMASVSVLGGGINSVQTLAMRL
 PFCGNINIFFACEILAVLKACADISLNITMVISNMAFLVPLMVFFYSMBILYTILOMNSATG
 RKAFTSCSAHLTVVIFGYGTIFFMYAKPKSQDLIGEELQLADKLSLIFYGVVTPMLNPILYSR
 NKDVKAAVKYLLNKKPIH (SEQ ID NO: 361)

ATGATTGTTCAAGTAATTTGTACTGTTGTTTCTTGGCAGTAAATACATTTCACTGTTAGATC
 TTTCTTTGATTCTGAAAGCAGATGACATGGGTGAGATTAAACAGACACTGTGTCAGAA
 TTTCTTCTTCTGGGTCTTCTCGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATCT
 55 AGTATGTACTAGTGATTCTAATTGGCAATGGTGTCTTAATCATAGCCAGCATCTTTGATT
 CTCAATTTACACACCAATGTACTTCTCTGGGCAACCTCTCTTCTCGGATATCTGCTAT
 ACATCTCTCTGTTCCCTCAACATTTGGTGAGCTTAATCTCAAGAAAGAAACATTTCTC

5 TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGAATGGGGTCAACAGAAATGTCTGCT
TCTTGGCATGATGGCAATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
ATCTGAGCAAGGTGGCGTATGTATTGATGGCTCTGTGTCTGGCTGTCGGTGGGAATAA
ATTCACTGTGCAAACTTACTTGCCATGAGACTGCCCTTCTGTGGGAATAATATTATCAA
10 TCATTTTCGATGTGAAATAATTAGCTGTCCCAAGCTGGCTGTGATATATCCCTCAATA
TATACCATGGTGATATCAAATATGGCCCTTCTGGTTTCTCCACTGATGGTCATTTTTTTC
TCCTATATGTTCATCTCTACACCATCTTGTGCAAAATGAATTGAGCCACAGGAAGACGCAAGG
CATTTTCCACAGTGTGCTCAGCTCACTGACTGGTGTGATCATATTTACGGTACCATCTCTTT
ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATGCAAGCATTAGAC
AAGCTCATTTCTGTGTTTATGGGGTAGTGACACCATGCTGAATCTTACTATCTATAGCTT
15 GAGAAATAAGGATGTAAAAGCTGCTGTAAATATTGCTGAACAAAAACCAATTCACTA
A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMTPEFLVFGTDYLPRLVTLFLVFLVYTLTMVGNILLILVNINSSLOIPMYVFLSNL
SFLDISCATITPKMLANFLASRKSISPGYCALQMFFFASFADAELILAAAMYDRYAICNPILL
YITLMSRRVVCVFVILVYFSGSTTSLVHVCLTFLRSLFCGNSNIVNHFFCDIPILLALSCDTQINQL
LLFALCCTGTSTFVVFIVISYFCLITVLSEKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
20 YSLDITDKVAVFYTVVFPMFNPHIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
ID NO: 363)

25 ATGTGTGGAGAGTAATACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC
TACCTCTAGAGAGTACACTGTTCTGGTATTCCTCTGGTATATACATTAACATATGGTCGGA
AATATACTCTAATAATTCTAGTTAATTAATTAACAGCCTTCAAATCCCATGTTATTTT
TCTTAGCACTTATCTTTCTAGACATCAGCTGTTCTACAGCAACTCACTCTAAATGCTGG
CAAACCTCTGTGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
CTTCGCTCTTTTGTGCTGATGCTGAGTGCCTTATCTGGCAGCAATGGCTTATAGCCGCTATG
CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGCTGTGTCTGTCT
CATTTGTGTGGCATATTTCACTGGAAGTACAACATCACTGGTGCATGTGTGCTCCACATT
30 AGGCTGTCAATTTGTGGCTCCAATATCGTCAATCATTTTCTGTGATATCCCACTCTCTT
GGCTITATCATGTACAGACACTCAGATCAACCAAGCTTCTGCTCTTGTCTTGTGCACTTCA
TCAGACAGCACTTTTGTGGTAATATTTATTTCTTACTCTGCATCCTACATGCTGTGGT
AGCATCAAGTCTCAGGTGGCAGAAGCAAAACATTCTCCACTGTGCTTCCCACCTCATAG
CAGTCACCTTATCTATGGAGCGCTCCTGTTATGTACTACAGCCCACTAGCTATTCC
35 CTAGACACTGATAAGTGGTGGCAGTGTTTTATACTGTTGATTTCCCATGTTTAATCCAA
TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
TGGATATTCAAAATGAATGGTATTTAAATCGTTTAAAGATAGTCAATATCTAA (SEQ ID NO:
364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHGMVVRTNESNLGFIILGFSIDYPQLQKVLVILILYLLTILGNTTI
ILVSRLEPKLHMPMYFFLSHLFLYRCFTSSVYQLLVNLWEPMKTIAYGGCLVHLYNSHALGS
TECVLLALMSCDRYVAVCRPLHYTVLMIHLCLMALASMAWLSGIATLTVQSTLTLQLPFCGH
RQVDHFICEVPLIKLACVGTIFNEAEFLVASILFLIVPVSEILVSSGYIAHVLRIKSATRRQAF
45 GTCFSLHTVVTIFYGTIIFMYLQPAKRSRSDQGFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
VLAKALGVNLI (SEQ ID NO: 365)

50 ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCTCTTTAGGGTTTCTGATTATCC
TCAGITACAGAAAGTTCTAATTTGTGCTCATATTGATCTGTATTTACTAACTATTTGGGGA
ATACCAACATCATCTGTTTCTCGTCTGGAACCCAAGCTTCATATGCCAGTATGATTTCTTC
CTTTCTCATCTCTCTCTGTAACCGTGCTTCCAGCAGTGTTATTCGCCAGCTCTGCT
AAACCTGTGGGAACCCATGAAAACATATGCCTATGGTGGCTGTTGGTTACACTTTACAAC
TCCCAATGGCTGGGATCCACTGAGTGCCTCTCTGGCTCTGATGCTGTGACCCGCTATGT
55 GGCTGTCTGCCGTCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCAATGGCCTTGG
CATCTATGGCATGGCTCAGTGGAATAGCCACCACCCTGGTACAGTCCACCCTACCCCTGCA

- GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTCATCTGCGAGGTCCCTGTGCTCATC
AAGCTGGCTTGTGTGGGCACCAAGTTTAAACGAGGCTGAGCTTTTGTGGCTAGTATCCTTT
TCCTTATAGTGCCTGTCTCATTTCATCTCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTG
AGGATTAAAGTCAGCTACCAGGAGACAGAAAGCATTGCGGACCTGCTTCTCCCACTGACA
GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCACGCCAAGAGTAGAT
CCAGGACCCAGGGCAAGTTTGTCTCTCTCTACACTGTGGTAACCCGCATGCTTAACCC
TCTATTATACCTTGGAGTCAAGGAGGTGAAAGGGCATTAAAGAAAGTTCTAGCAAA
GGCTCTGGGAGTAAATATTTATGA (SEQ ID NO: 366)
- 10 **AOLFR198 sequences:**
MENCTEVTKFILLGLTSVPELQIPLFILFTFYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQFFFVALATVENYLLASMA YDRYA AVCKP
LHYTTTMTASVGCALALGSYVCGFLNASFHIGGIFLSFCCKSNLVHHFFCDVPVAMALSCSDKH
TSEVILVFMSSNFIFVLLVIFISYLFIFITILKMHSAGHKALSTCASHFTAVSVFYGTVIFIYQL
PSSSHMSMDTKMASVFYAMIIPMLNPVVYSRLNRREVQNAFKVLRRQKFL (SEQ ID NO: 367)
- 20 ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCAGAAC
TACAGATCCCCCTTTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
GGGATGATGTGTGCTGATCCTGATGGACTCTTGCTCCACACCCCCATGTACTTTTCTCTCAG
TAACCTGTCTCTGTGGACTTTGGATACCTCCTCAGCTGTCACTCCCAAGGTGATGGCTGGG
TTCCTTAGAGGAGACAAAGGTCACTCTCTACAAATGAGTGTGCTGTTCAGATGTCTTCTTTGT
AGCCTTGGCCACCGTGGAAAAATTACTTGTGGCTCAATGGCCATATGACCGCTATGACGCA
GTGTGCAAAACCCCTACACTACACCACCACCATGACGGCCAGTGAGGTGCTGTCTGGCC
TAGGCTCATATGTCTGTGGCTTCTCAAATGCCTCATTCACATTTGGGGGCATATTCAGTCTC
TCTTCTGTAAATCCAATCTGGTACATCACTTTTCTGTGATGTCCAGCAGTCATGGCTCT
GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTATGTCAAGCTTTAATATCT
TTTTGTCTCTTAGTATCTTTATCTCCTACTTGTTCATATTCATCACCATTCTGAAGAGTCT
ATTCAAGTAAAGGACACCAAAAAGCAATTGTCCACCTGTGCCTTCACTTCACTGAGCTCTC
CGTCTCTATTTGGGACAGTAATCTTCATCTACTTGCAGCCAGCTCCAGCCACTCCATGGAC
ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCACTCCCATGCTGCAACCCCTGTGGTGT
ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCAAAAAT
TTCTATAA (SEQ ID NO: 368)
- 30 **AOLFR199 sequences:**
MDTGKNTLPQDFLLGFPQSQTQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
NLSFLEIWTYTAAPVKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLAAMAYDRCLAICY
LHYGAIMSSLLSALQALGSWVCGFVIAVPTALISGLSFCGPRAINHHFCDIAPWIALACINTQA
VELVAFVIAVVVILSCITLTFVSYYIITLIRPSAGRSKAFSTSSHLTVVLIWYGSTVFLHVR
TSIKDALDLIAKAVHLNLTVPVLPVLPNFIYTLRNEKRETLLEKWKKG (SEQ ID NO: 369)
- 40 ATGGACACAGGCAACAAAACCTGCCCCAGGACTTCTCTTACTGGGCTTTCCTGGTTCTC
AAACTCTTCAGCTCTCTCTCTTTATGCTTTTCTGGTGTATGATCCTCAGAGTATAGTGGT
AATGGGCTATCTTGTATGTGGTGAGCACCTCCCATCAGTTGCATACCCCCATGTACTTCT
TCTGAGCAACCTCTCCTTCTCTGGAGATTGGTATACCACAGCAGCAGTGCCTCAAGGACTG
GCCATCTCTACTGGGAGAGTCAAGCCATATCATTTACAAGCTGTCTTTGAGATGTACT
TGTTTTCTCAITTAGGCTGCACAGAGTACTTCTCTGGCAGCCATGGCTATGACCGCTGT
CTTGCCATCTGCTATCTCTTACACTACGGAGCCATCATGAGTAGCCTGTCTCAGCGCAGC
TGGCCCTGGGCTCTGGGTGTGTGGTTTCTGGGCCATTGACGTGCCACAGCCCTCATCAG
TGGCCTGTCTCTGTGGGCCCTGTCATCAACCACTTCTCTGTGACATTGACCCCTGGA
TGGCCTGGCCTGCACCAACACACAGGAGTATGAGCTTGTGGCCTTTGTGATGTGCTGTTGT
GTTATCTCTGAGTTTCATGCTCATCACTTGTCTCTATGTGTACATATCAGCACCATCTC
TCAGGATCCCTCTGCGAGTGGCCGGAGCAAGCCTTCTCCACGTCTCTCGCATCTCAC
CGTGGTGTCTCAITTTGGTATGGGTCCACAGTTTCTTCTCAGCTCCGACCTCTATCAAGAT
GCCTTGGATCTGATCAAGAGTGTCCACGCTCTGAACACTGTGGTGACTCCAGTTTAAACC
CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

- MTRKNYTSLETFVLLGLADTLELQILFLFFLVIYTLTVLGNLMILLIRIDSQHLTPMYFFLANL
SFVDVNCNSTITPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
5 YSLIMSRITYYLKMAAGAFAGLLNFMVNTSHVSSLFCDNSVHHFFCDSPPLFKLSCLSDTLKE
SISSILAGVNIIVGTLVLVILSSYSYVLSFISFMHSIGEGRHRAFSTCASHLTAILFYATCIYTYLRPSS
SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRSTSFL (SEQ ID NO: 371)
- ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGG
TGGAGCTACAGATTACTCTCTTTTGTITTTTCTTGTGATTATACACTACAGTACTGGGA
10 AATCTCGGGATGATCTCTTAATCAGGATCGATTCCCGAGCTCACACACCCATGTATTCTT
CCTGGCTAACCTGTCCTTTGTGGACGTTTGAACCTCAACTACCATACCCCAAGATGCTG
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTTGTGGCTGCTTCTACAGATGTA
TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTTAATGGCCTATGACAGGTA
15 TGGCGCCATATGTGCGCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGCTACACATAAA
ATGGCAGCCGGGGCTTTTGTGTCAGGGTTGTGAACTTCATGGTCAACACAAAGCCATGCA
GCAGCTTGTCACTTGTGACTCCAATGTCATCCATCACTTCTTGTGACAGTCCCCCACTT
TTCAGGCTCTCTTGTCTGACACAATCCTGAAAGAAAGCATAAAGTCTATTTTGGCTGGTG
TGAATATTGTGGGACTCTGCTTGTCACTCTCTCTCTACTCTACGTTCTCTTCTCCATT
20 TTTTCTAGCATTCGGGGAGGGGAGGCACAGAGCTTCTCCAGGTGGCTCTCACTGA
CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCAGCTAC
TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC
CTCTGATCTACAGCTCAGGAGTAAGGAAGTAAAGAAAGGCTTAGCGAATGTAATTAGCA
GGAAAAGGACCTCTTCTCTCTGTA (SEQ ID NO: 372)

AOLFR201 sequences:

- MEWENHTLVEFFLKGLSGHPRELELFFVLIFIMYVILLNGNTLILISILDPHLHTPMYFFLGNL
SFLDICYTTSISPTLSVLSERKTISLSCAVQMFLGLAMGTTECVLLGVMAFDRYVAICNPLR
YPIIMSKDAYVPMAGSWIIGAVNSAVQSVFVQVLPFCRNNIINHFTCEILAVMKLACADISDN
30 EFIMLVATTLFILPLLLIIVSYTLIHSIFKISSSEGRSKASSTCSAHLTVVIFYGTILFMYMKPKS
KETLNSDDL DATDKIISMFYGVMTMNMNPLIYSLRNKDVEAKVHLLNRRFFSK (SEQ ID NO:
373)
- ATGGAATGGGAAAACCAACACCATTTCTGGTGGAATTTTTCTGAAGGACCTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTTGTGCTCATCTTCATAATGTATGGTGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAAATCAGCATCTTGGACCTCACTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACTCTATAGCTCCACCGCTAG
TGAGCTTCCTTTCAGAAAAGAACCATTTCCCTTTCTGGCTGTGACGTGCGAGATGTTCTC
35 CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
GTGGCATCTGCCAACCTCTGAGATATCCCATCATGATGATAGGATGCCTATGTACCCA
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCATCAACATCAGTGTGTTTGGT
ACAATTGCTCTTCTGCAGGAATAACATCATCAATCATTTCACTGTGAAATTTCTGGCTGTC
40 TGAACACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
TGTTTCATATTGACACCTTTGTTATTAATCATTTGCTCTTACACGTTAATCATTTGTGAGCATC
45 TTCAAAATTAGCTTCTCCGAGGGGAGAGAAGCTTCTCTACCTGTTTACGCCCATCTGA
CTGTGGTCATAATATTCTATGGGACCATCCTCTTCACTGTACATGAAGCCCAAGTCTAAAGA
GACACTTAATTCGGATGACTGGATGCTACCGACAAAAATTATATCATGTTCTATGGGGTG
ATGACTCCCATGTAATCCTTTAATCTACAGTCTTAGAACAAGGATGCTTAAGAAAGGGCA
GTAAAAACCTACTGAACAGAAGGTTCTTAGCAAGTGA (SEQ ID NO: 374)

AOLFR202 sequences:

- MEWENHTLVEFFLKGLSGHPRELELFFVLIFIMYVILLNGNTLILISILDPHLHTPMYFFLGNL
SFLDICYTTSISPTLSVLSERKTISLSCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR
YPIIMSKDAYVPMAGSWIIGAVNSAVQTVFVQVLPFCRNNIINHFTCEILAVMKLACADISGN
55 EFILLVTTTLFLLPLLLIIVSYTLIILSIFKISSSEGRSKPSSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDATDKLIFYRVMTPMMNPLIYSLRNKDVKEAVKHLHRRKNFNK (SEQ ID NO: 375)

ATGGAATGGGAAAACCAACACCATTTCTGGTGGAAATTTTTCTGAAGGGACCTTCTGGTCACC
5 CAAGACITTGAGTTACTCTTTTTTGTGCTCATCTTCATAATGTATGGTGCATCCTCTCGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCTTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAAACCTCTCCTTCTTGACATCTGCTACACACCACCTCTATCCCTCCACGCTAG
TGAGCTTCCCTTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCCT
10 CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGTATGGCCCTTTGACCGCTAT
GTGGCTATCTGCAACCTCTGAGATATCCCATCATCATGAGTAAGGATGCCATGTATGCCA
TGGCAGCTGGGTCTCGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTITGTGGT
ACAATTGCCTTCTGCGAGGAATAACATCATCAATCATTACCTGTGAATTTCTAGCTGTG
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCACCTCTGCTGTGACCCACAACAT
15 TGTTCCTATTGACACCTTTGTATTAAATATTGTCTCTTACACGTTAATCATTITGAGCATC
TTCAAAATTAGCTCTTCGGAGGGGAGAAAGCAACCTCTCTACCTGCTCAGCTCGCTGA
CTGTGGTGATAAATCTCTGTGGGACCACTCTCCCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATCAGATGAACTTGGATGCCACTGACAACTTATATTCATATTCTACAGGTG
ATGACTCCCATGTGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
GTAAACACCTACTGAGAAGAAAAATTTTAAACAGTAA (SEQ ID NO: 376)

20 **AOLFR203 sequences:**

MRQRNQSCVVEFILLGFSNFPELQVQLFGVFLVIYVVTLMGNAITVIISLNQSLHVPMYLFLLN
LSVVEVSFAITPEMLVVLSTEKTMISFVGCFAQMYIFFLGGTECFLLGLGAMAYDRFAAICHPL
25 NYPVIMNRGLVMFKLVIFSWISGIMVATVQTWVFSFPCGPNINHLCETPPVLELVCAIDTFLF
EYIAFTGRLIVMPFLLILLSYIRVLFAILKMPSTTGRQKAFSTCASHLTANVTYLFYGTANMTYLO
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRTLKLRWRKVILHTF (SEQ ID NO: 377)

ATGAAAGACAAATCAAAGCTGTGTGGTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
30 CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCCTAGTATTATATGTGGTGACCTGAATGGG
AAATGCCATATTACAGTCATCATCTCTTAAACAGAGCCCTCCAGTCTCCCATGTACCTGT
TCTCTGCAGCACTATCTGTGGTGGAGGTGAGTTTCTGCGAGTCATGACCTGAAATGCT
GGTGTGTCTCTACTGAGAAACATGATTTCTTTTGTGGGCTGTTTGCACAGATGTAT
TTCATCCTCTCTTTTGTGGGACTGAATGTITTTCTCGGGAGCGATGGCTTATGACCGATT
35 TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTATGAAA
TTAGTAATATTCTAGGATCTCAGGGATCATGGTGGCTACTGTGCAGACAGTCTGGGTAT
TTAGTTTTCATTTTGTGGCCCCAATGAAATTAATCATCTCTCTGTGAGACTCCCCGGTA
CTAGAGCTGTGTGTGCAGACACCTTCTTATTGAAATCTATGCCCTACAGGCACCATTTT
GATTGTTATGGTTCTCTTCTGTGTGATCCTCTGTCTTACATTCGAGTCTGTTTGGCATCCT
40 GAAGATGCCATCAACTACTGGGAGACAAAGGCCCTTTCCACCTGTGCCCTCACCCTCACA
TCTGTGACCCTGTCTATGGCAGACGCAATATGACTATTATACACCAAACTTGGCTACTC
ATCCGAACCAAGAAATGATCTCATTTGGCTTACAGCTGTGTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAAGTGAAGGACTTGTATAAATATGTGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

45 **AOLFR204 sequences:**

MEKKKNVTEFILGLTQNPIMEKVTFVVFLVLYMITLSGNLLIVVTTTTSQALSSPMYFFLTHLSL
IDTVYSSSAPKLIVDSFQEKKIISFNGCMAQAYAEHIFGATEIILLTVMACDCYVAIKPLNYTT
IMSHSLCILLVAVWVGGLFHAITQILFTVWLPFCGPNVIGHFMDLYPLLKLVCIDHTLGLFV
50 AVNSGFICLLNFLILVSVYIHLRLKNSLEGRCKALSTCISHIIVVVLFFVPCIFVYLRSTILPI
DKAVAVFYTMVVPMLNPVVYTLRNAEVKSAIRKLWRKKVTSND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCAT
ATGGAGAAAGTCAGCTTTGTAGTATTTTGGTTCCTTACATGATAACACTTTCAGGCAACC
TGCTCATTTGGTGTACCAATACCACAGCCAGGCTCTGAGCTCCCCATGTACTTCTCTCGT
55 ACCCACTCTTTTGTATAGACACAGTTTATCTCTCTCAGCTCTAAGTTGATTGTGGA
TTCCTTTCAAGAGAAGAAATCATCTCCTTTAATGGGTGATGGCTACAGGCTATGCAGAA

CACATCTTTTGGTGCTACTGAGATCATCTCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG
CCATCTGCAAAACCTCTGAACTACACAACCATATGAGCCACAGCCTGTGCATTCCTCGGT
GGCAGTGGCCTGGGTGGGAGGATTTCCTCATGCAACTATTACAGATTCCTTTACAGATATGG
CTGCGCCTCTGTGGCCCAATGTCATAGGCCACTTCATGTGTGACTGTGACCCATTGTATAA
1 5 ACTTGTTGGCATAGACACTCATACCCCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT
GCTTATTAACACTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC
AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTACATCATAGTAGTGG
TCITATTCCTTGTGCCCTGTATATTGTGTATCTCGCGCTCAGTGACCACTCTGCCCATGTAT
10 AAAGCTGTTGCTGTATTTTATACTATGTTGGTGGTCCCAATGTATAAATCCCGTGGTCTACACAC
TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAGTGACTTCAG
ATAATGATTAA (SEQ ID NO: 380)

AOLFR205 sequences:

MESENRTVIREFILLGLTQSQDIQLLVFVLVIFYFILPGNFIIFTIKSDPGLTAPLYFFLGNLAF
15 DASYSFTVAPRMLVDLFAKKIISYRGCTQLFHLHFGGGEGLLLVMAFDRYIAICRPLHYPT
VMNPRCTYAMMLALWLGGFVHSIIQVVLILRPLFCGPNQLDNFFCDVPQVIKLACTDTFVVEL
LMVFNSGLMTLLCFLGLLASYAVILCRIRGSSSEAKNKAMSTCTHHIVFMFGPIFYTRFPRA
FPADKVVSLFHTVIFPLLNPVIYTLRNQEVKASMKKVFKNKHIA (SEQ ID NO: 619)

20 ATGGAAAGCGAAGAACAGACAGTGATAAGAGAATTCTACTCTCTCTGCTGACCCAGTCT
CAAGATATTCAGCTCCTGGCTTTGTGCTAGTGTAAATATCTTACTTCATCATCTCCTCGG
AAATTTTCTCATTATTTACCATATAAGACAGACCTGGGCTCACAGCCCCCTCTATTCTT
TTCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCTTCACCTGGGCTGGGCTCCGGATGTG
GTGGACTTCTCTCTGCGAAGAGATAATCTCTACAGAGGCTGCATCACTACGCTCTTTT
25 TCTTGCACTTCTTGGAGGAGGGAGGGATTACTCCTGTTGTGATGGCCTTTGACCGTCA
CATCGCATCTGCGCGCCTCTGCACTATCTACTGTGATGAACCTAGAACCTTGCTATGCA
ATGATGTTGGCTCTGTGGCTTGGGGGTTTGTCCACTCCATTATCCAGGTGGTCCCTACTCT
CCGCTTGCTCTTTTGTGGCCCAACACAGCTGGACAACTCTCTGTGATGTCCCAAGCT
ATCAAGCTGGGCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGGTGGC
30 TGATGACACTCTGTGCTTTCTGGGGCTTCTGGCCTCTATGCAGTCATTTTGTGCGATA
CGAGGGTCTTCTCTGAGGCAAAAAACAGGCCATGTCCACGTCATCAACCATATCATATTG
TTATATCTTCTCATGTTTGGACCTGGCATCTTCACTACACGCGCCCTTCAGGGCTTTCCCA
GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTCTCTTGTGTAATCTGTCAATTA
TACCTCTCGCAACCGAAGGTGAAAGCTTCCATGAAAAAGGTGTTAATAAGCACATAGC
35 CTGA (SEQ ID NO: 382)

AOLFR206 sequences:

MANRNNVTEFILLGLTENPKMQKIIFVFSVIYNAMIGNVLIVVTITASPSLRSPMYFFLAYLSFI
40 DACYSSVNTPKLITDSLYENKILFNGCMTQVGEHFFRGVEVILLTVMAYDHYVAICKPLHYT
TIMQKHVCSLLVGVSWVGGFLHATIQILFIQCLPFCGPNVIDHFMCDLYTLINLACTNHTLGLF
IAANSGFICLLNCLLLVSCVVILYSLKTHSLEARHEALSTCVSHITVILSIFICFIVMRPPATL
PIDKAVAVFYTMTSMNLNPLIYTLRNAQMKNAIRKLCRSKAISSVK (SEQ ID NO: 383)

45 ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA
ATGCAGAAAATCATATTTGTTGTGTTTCTGTGCATCTACATCAACGCCATGATAGGAATG
TGCTCATTTGGTGACCATCACTGCCAGCCCATCAGAGATCCCCATGTACTTTTCTGT
GCCTATCTCTCTTATTTGATGCTGCTATTCTCTGTCAATACCCCTAAGCTGATCAGATA
TTCACCTATGAAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGCTCTTGGAGAA
CATTTTTCAGAGGTGTTGAGGTGATCTCACTTACTGTAATGGCCTATGACCATCTATGGG
50 CCATCTGCAAGCCCTTGCACTATACCACCATCATGAAGCAGATGTTGTAGCCTGTGATG
GGGAGTGCATGGGTAGGAGGCTTTCTCATGCAACCATACAGATCCTCTTCATCTGTCAA
TTACCTTTCTGTGGTCTTAATGTGCATAGTCACTTTATGTGTGATCTCTACCTTTGATCAA
TCTTGCCCTGCACTAATACCCACACTCTAGGACTCTCAATGGTGCACCAAGCTGGGTTCATAT
GCCTGTAAACTGTCTTGTCTCTGCTCTCGCTGGTGCATCATGTACTCTTAAAGAAC
55 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCACTGTGTCTCCCACTACAGTGTGTCA
TCTTATCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAAATGAAAAATGCCATTAGGAAATTTGTGTAGTAGGAAAGCTATTTCAGG
TGCAAAATA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSEFFVLGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIFDLSHLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVMAAAGSWVTGLVDVSVVQTAFAAMQLPFCANNVIKHFEVCEILAILKLACADI
SINVISMTGSNLIVLVIPLVISISYIFIVATILRIPSTEGKHAFSTCSAHLTVVIFYGTIFFMYAKP
10 ESKASVDGSDNEJIEALISLFYGVMTPLNPLIYSLRNKDVKAAVNILCRKNFSDGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAAATTTTCTGGTAGGGCTTTCTGCCACC
CAAAGCTCCAGACAGTTTCTCGTTCTAAATTTGTGGATGTACCTGATGATCCTGCTTGGAA
15 ATGGAGTCCATTATCTCAGTTATCATCTTTGATTCTACCTGCACACCCCCATGTATTCTT
CCTCTGAATCTTTCTTCTCGACGTTTGCTACACAAGTTCTCTGTGCCACTAATTCTGT
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGCAAAATGTTAT
TTCCTTTGCCATTGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCAT
20 GTGGCCATCTGCTACCCACTGAGATACCTCTGCATCATGAGCAAGGGTGCCATGTGGCCA
TGGCAGCTGGGTCTGGGTCACTGGGCTTGTGGACTCAGTAGTGACAGACAGCTTTGCAAT
GCAGTTACCAATCTGTGCTAAATAATGTCAATAAACATTTTGTCTGTGAAATCTGGCTATCT
TGAACATGGCCTGTGCTGATTTCAATCAATGTGATTAGTATGACAGGGTGCAATCTGAT
TGTTCTGGTTATTCACATTGTAGTAAITTCATCTCTTACATATTATTGTGTGCCACTATCT
GAGGATTCCTTCCACTGAAGGAAACATAAGGCCCTTCTCCACTGCTCAGGCCACTGACA
25 GTGGTGATTATTCTCATGGAACCATCTTCTCATGTACGCAAAAGCTGAGTCTAAAGCCT
CTGTTGATTACAGGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCTCTCATCTATAGTCTGCGAAAAACAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAACTTTCTGATGAAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTVCQIAAGSWMTGCLTAMVEMMSVLPPLSLCNSIINHFTCEILAILKLVCVDTS
LVQLIMLVISVILLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFYGTALSMH
35 LKPSADVQSEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKKLIRNHNFATFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAAATGGACATCTGTAAAAGTATTTTCTTCTGGGATTTTTCCTACTACC
CAAAGTTCAGGTTCATCATATTTGCGGTGTGCTGTGATGTACCTGATCACCTGTGCTGGGC
40 AACATTTTCTGATCTCCATCACCATTCTAGATTCCCACTGCACACCCCTATGTACCTCTT
CTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTTCTTGCCTCTCTCCAATCTGCG
CAAATCTTTGTTTCAGGGAGAAACACTATTTCATTCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATACCTGTCTCATGATGAATGAGGAACCTGTGTGCAGA
45 TTGCAGCTGCCTCTGGATGACAGGCTGTCTCACTGCCATGGTGAAATGATGTCTGTGCT
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTTCACITGTGAAATCTTGCCCATCT
TGAATTTGGTTGTGGGACACTCCCTGGTGCAGTTAATCATGCTGGTGCATCAGTGATCT
TCTTCTCCCCATGCCAATGCTACTCAATTTGATCTCTATGCAATTTATCTCGCCAGTACTC
TGAGAATCAGCTCAGTGAAGGTCGAAGTAAAGCCTTTTCAACGTGCACAGGCCACCTGA
50 TGGTGGTGAATTTGTGTTCTATGGGACGGCTCTCTCCATGCACTGAAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT
CCTATCATTAATGCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATGCTGATTAA
GAAATCATTTTAATACTGCCTTCATTTCATCCTCAATAA (SEQ ID NO: 388)

09866055-062201

095605-06204

AOLFR209 sequences:

MDKINQTFVREFILLGLSGYPKLEIIFFALILVMYVVLIGNVGLIILASILDSRLHMPMYFFLGNLS
5 FLDICYTITSSIPSTLVLSISKRNISFSGCAVQMFQFAMGSTEFCFLGLMMAFDTRYVAICNPLRY
PIIMNKVVVYVLLTSVSWLSGGINSTVQTSLAMRWPCFQNNIINHFLCEILAVLKACSDISVNV
TLAVSNI AFLVPLLVIFFSYMFILYITLRN SATGRHKA FSTCSAHLTVTVIIFYGTIFFMYAKPKS
QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAIAKLYLLSRKAINQ (SEQ ID NO:
389)

10 ATGGACAGAATAAACCCAGACATTGTGAGAGAATTCATTCTCTGGGACTCTCTGGTTACC
CCAAACTTGAGATCATTCTTTCTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
AATGGTGTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTACATGCCCATGTCACTCTCT
15 CTTGGGCAACGCTCTCTTTCTTGGGATATCTGCTATACAACTCTCCATCCCTCAACACTGG
TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCAGATGTTCTT
TGGGTTTGCAATGGGGCTCAACAGAAATGTTCTCTCTTGGCATGATGGCATTGTATCGTTAT
TGCGCCATCTGTAACCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
TGACTTCTGTATCATGGCTTTCTGGTGGAATCAATCAACTGTGCAAAACATCACTTGCCAT
GCGATGGCTTTCTGTGGGAACAATATTATTAATCAATTTCTTATGCGAGATCTTAGCTGTC
20 TAAAATTAGCTTTGCTGATATATCTGCAATATTGTTACCCTAGCAGGTGCAAAATATTGGT
TTCTTAGTTCTCTCTCTGCTCGTGATTTTTTCTCCTATATGTTTCACTCTCAACCATCTGT
CGAACGAACCTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
TGGTGATCATATTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCGAGGACCTC
CTTGGGAAAGCAAACTTGCAAGCTACAGAGGGGCTGTGTTCATGTTTATGGGGTGTGGA
25 CCCCCATGTTAAACCCCATATCTATAGCTTGAGAAATAAGATGTAAAAGCTGCTATAAA
ATATTTGCTGAGCAGGAAAGCTATTAAACCAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

MMGRNRDNTNADFILTGLSDSEEVQMALEFMLFLIYLLITMLGNVGMILLIRLDLQLHTPMYFFL
30 THLSFIDLSTYSYVTPKLTANLLTSNYISFTGCF AQMF CFVFLGTAE CYLLSSMAHYDRYAACSP
LHYTVIMPKRLCLALITGPYVIGFSDSFNVVMSRLHFVDSNIIHFFCDTSPILASCTDND
TEMLIFLAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTFIFYGTIMFYTLKP
RKSYSYLG RDQVAPVFTYITVPLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
35 TCTGAAGAGGTCAGATGGCTCTGTTTATGCTATTTCTCTCATATACCTAATTACTATGCT
GGGGAATGTGGGGATGCTATTGATAATCCGCTTGGACCTCCAGCTCACACTCCCATGTAT
TTTTCTCTTACTCACCTGTCATTTATGACCTCAGTTACTCAACTGCTGTCACACCTAAAAAC
CTTAGCGAAGCTTACTGACTTCCAACATAATTTCTTACCGGGTGTCTTGCCCGAGATGTTCT
GTTTGTGTTCTTGGGTAAGTCTGCTGAATGTTATCTTCTCTCAATGGCCTATGATCGCTAT
40 CGAGCGATCTGCAAGCTCTCACTACACAGTATTATGCCCCAAAGGCTATGCTCGCTC
TCATCACTGGGCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
AGATTGCATTTCTGTGACTCAAAACATAATTCATCACTTTTTCTGTGACACTTCCCAATTG
AGCTCTGTCTGCAGCTGACACAGACAACACTGAAATGCTGATTCATTATCGCTGGTTC
ACCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTACCATCCT
45 GAAAATTAATTCACCTTCAAGAAAGCAGAAAGCTTTCTCTACTTGGCTCTCTCATCTCTTG
GGAGTCACCATCTTCTATGGAATATGATTTTTACTTACTTAAAGCCAAGAAAGTCTTATT
CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACATATTGTGATCCCATGCTGAATCC
ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

AOLFR211 sequences:

MMGRNRNTNADFILMGLTSEEIQMALEFMLFLIYLLITMLGNVGMILLIRLDLQLHTPMYFFL
35 THLSFIDLSTYSYVTPKLTANLLTSNYISFTGCF AQMF FFLGTAE CYLLSSMAHNDRYAACSP
LHYTVIMSKRLCLALITGPYVIGFISDFNVVMSRLHFYDSNVIIHFFCDTSPILASCTDTPKNT
EILFIIVGSTLMVSLITISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTFIFYSTLIFYTLKRY
SYSYLG RDQVASVFTYITVPLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
 GGGAAATGTGGGGATGATATTGATAATCCGCTGGAGCTCCAGCTTCGACACTCCCATGTATT
 5 TTTTCTTACTACCTGCTCATTTATTGACCTCAGTTACTCAACTGTCGCTACACATGAACCT
 TTAGCGAACTTACTGACTTCCAACCTATATTTCTTTCACGGGCTGCTTTGCCAGATGTTCTT
 TTTTGCTCTTTGGGATGACTGCTGAATGTTACCTTCTCTCCTCAATGGGCCATGATGCGCTATG
 CAGCGATCTGCAGTCCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
 CATCACTGGGGCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
 10 GTTGGCATTTCACGACTCAAACGTAATTCACACTTTTCTGTGACACTTCCCAATTTTAT
 GCTCTGCTCGCACTGATACATACAACACGAAATCCTGATATTCAATTATGTGGTTCAC
 CCTGATGGTGTCCCTTTTACAATATCTGCATCTTATGTTTCATTCTTTACCATCTGTA
 AAATTAATTCCTCTCAGGAAAAGCAGAAAGCTTTCTCTACTTGGGTCTCTCATCTCTGGG
 AGTCACCATCTTTATAGCACTCTGATTTTACTTATTTAAACCAAGAAAGTCTTATTCTCT
 15 TGGGAAGAGATCAAGTGGCTTCTGTTTATATACTATTGTGATCCCGTCTCATCAATCCCAT
 CATTTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG
 ACGAGTACCAAGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFEVTVFLSGFANHPQLQVSLFLMFLFIYFLVTLGNLGLTLIRMSQLHTPMYFFLSN
 LAFIDIFYSSVTPKALVNFQSNRRSISFVCGFVQMYFFVGLVCCCEFLGSMAYNRYIAJCNPL
 LYSVVMQKVNWLGVMPYVIGFTSSLSVWVISSLAFCDSSINHFFCDTALLALSCVDTFGT
 EMVSFVLGFTLLSSLITVTYIIIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGLIFTYLPQD
 NTSSLTQAQVASVFYTVIIPMLNPLIYSLRNKDVKNALLRVIHRKLP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCTATCCTCTCTGGATTGCAAAATCAC
 CTGAATTACAAGTCAGTCTTTCTTGATGTTTCTCTTCATTATCTATTCAGTGTTTGGGA
 AACCTGGGACTGATCAGGTTAATCAGAATGGATTCTCAGCTCAGCAACCCCTATGTACTTTT
 TCTCGAGCAATTATGACATTATTGACATATTTACTCCTCTACTGTAACACCTAAGGCAATG
 30 GTGAATTCCAATCCAATCGGAGATCCATCTCCTTTGTGGCTGCTTTGTCAAATGTAATT
 TTTGTGTGATTGGTGTGTTGTGAGTGTTTCTCTGGGATCAATGGCCTACAATCGCTACA
 TAGCAATCTGCAATCCCTTACTGTATTCACTAGTCATGTCCTCAAAAAGTGTCCAACCTGGCT
 GGGAGTAATGCCATATGTGATAGGCTTCAACAGCTCGCTGATATCTGTCTGGGTGATAAGC
 AGTTTGGCGTTCGTGATTCCAGCATCAATCAATTTTTTGTGACACCAAGCTCTTTTAGC
 35 ACTCTCTGTGTAGATACATTCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
 CTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCATCTCAGCCATCTCTGAG
 GATCCAGTCAGCAGCAGGCGAGGAGGAGGAGGCTTCTCCACCTGCGCATCCCACTATGGCT
 GTAACTATCTTTATGGGTCTCTGATTTTACCTATTGTGAACCTCATACAACACATCATGCT
 40 GACCAAGCGCAGGTGGCATCTGATTCTATACGATTGTCAATCCCATGCTGAATCCACTCA
 ATCTACAGTCTGAGGAACAAGATGTGAAAAATGCTCTCTGAGAGTCATACATAGAAAA
 CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFS
 EAVLFYVLFVLYLLTLVGNFTIIISYLDPLHPTMYFFLSNLSDICFTTSLAPQTLVNLQRPKK
 TITYGGCV AQLYISLALGSTECILLADMALDRYIAVCKPLHYVIMNPLRQQQLASISWLSGLA
 SSLIHATFTLQLPCGNHRLDHFICEVPALLKLACVDTTVNELVLFVSVLFPVIPPALISISYGI
 TQAVLRIKSVEARHKAFTSCSHLTVVIIIFYGTIIYVYLQPSDSYAQDQKGFIISFYMTVPTLNL
 50 IYTLNRNKMKEALRKLLSGKL (SEQ ID NO: 397)

ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
 ATTTAATTGTTTGGAGTACCAATCCATCTCGCTTAGGTGCGGATCCCCGTGAGGG
 ATGGGATTGGGCAATGAGAGTTCCTCAATGGATTTCATCCTTCTAGGCTTCTCAGACCACC
 CTGCTCTGGAGGCTGTTCTCTTGTATTGTCTTTCTCTTCACTCTGACCTCTGTGGGA
 55 AACTTACCATAATCATCATCTCATATCTGGATCCCCCTTCATACCCCAATGTAATTTT
 TCTCAGCAACCTCTCTTACTGGACATCTGCTTCACTACTAGGCTTGCTCCTCAGACCTTAG

ATATCATTGAGCTGTTTCCTGGCTTAAATTAATTCCTACACCATCATTTTGATCGGTGTCGG
ATGCAGGTCCCTCAGTGGGTCATCTAAGGCTCTTTCTACATTAACTGCCACATCACAGTG
GTCATCTTTCTTCGGGCTTGCAATTAATTCATATATGGCTTTTAGACAGACTCTCGTG
GGACAAATTTCTTCTGTGTTCTACACTGTTGTACTCCCTTGTGAACCCCATCATCTACT
5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAAC
CCTGGAATACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLNSWELQMFFMVFSLLYVATMVGNLSLIVTVIVDPHLHSPMYFL
10 TNLSDMSLASFATPKMITDYLTHGKTSISFDGCLTQIFFLHLFTGTETILLMAMSFDRYIAKCP
HYASVISPQVCVALVYASWIMGVMHMSQVIFALTPFCGPYEVDSEFCDLPVVFQALACVDY
VLGLFMISTSGHIALSCFIVLNSYVIVLVTVKHHSSRGSSKALSTCTAHFIVVFLFFGPFIFIMY
PLSFLTDKILSVFYTIFPTLNPYITLRNQEVIAMRKLNRFLNFKAMPS (SEQ ID NO: 403)

ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGTCTGGGGCTCTCTAATTCCT
GGGAACACAGTGTTTTCTTTATGGTGTTTTCATTGCTTTATGTGGCAACAATGGTGGG
TAACAGGCTCATAGTCATACAGTTATAGTGGACCTCACCTACACTCTCTATGTATTTC
TGCTTACCAATCTTTCAATCATGATATGTCTCTTGCTCTTTGCCACCCCAAGATGATT
ACAGATTACCTAACAGGTCACAAAACCATCTCTTTGTATGGCTGCTTACCCAGATTTCT
20 TTTCCACCTTTTCACTGGAACAGAGATCATCTTACTCATGGCCATGTCTCTTGATAGGTAT
ATTGCAATATGCAAGCCCTGCACATGTCTCTGTCTTGTGACCTCCCAAGGTGTGTGTGCT
CGTGGTGGCTTCTGGAATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTGGCCCT
ACGTTACCATCTGTGGTCCCTATGAGGTAGACAGCTTTTCTGTGACCTTCCGTGGTGT
CCAGTTGGCTTGTGTGGATCACTATGTCTGGGCTCTTTATGATCTCAACAAAGTGGCATA
25 ATGCGTTGTCTGTTTTATTTATTTATTTAATTCATATGTTATGTCTGGTGTGGA
GCATCATCTTCCAGAGGATCACTAAGGCCCTTCTACTTGTACAGCTCATTTCAATTGTG
TCTTCTGTCTTTGGGCCATGCATCTTCACTACATGTGGGCCATAAGCAGCTTTCTCACA
GACAAGATCTGTCTGTGTGTATATCAACATCTTTACTCCACTGTGAACCCAATAATCTATAC
TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAACTGAAAAATAGGTTCTAAATTT
30 TAATAAGGCAATGCCCTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSLELQIFYLFFSVIYAATVLGNLLIVVTIASEPHLH
SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAISEFGCMQMFHLHLLGGAEIVLLISMSE
35 RYVAICKPLHYLTIMSRMCVGLVLSWIVGIFHALFTVNLPCFPGNEVDSFFCDLPVVK
LACVDTYLGVFMISTSGMIALVCFILLVISYTHLVTVRQRSSGGSSKALSTCSAHFTVTVLFFGP
CTFIYVWPFNTNPDKVLVSVFYTHYTPLNPIYTVRNKDKVYSMRKLSSHFHFKSRKTDHPT
(SEQ ID NO: 405)

ATGCTAGAGTCTTCCAGAAATCAGAGCAAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
GAATTCATACAGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTCTCGTGT
CTCCATAGTCTATGACGCCACTGTGCTGGGGAACCTTCTATTGTGGTCACCAATGCATCA
GAGCCACACCTTCAATCTCCCTACGTACTTTCTGCTGGGCAATCTCTCTTCAATGACATGT
CCTGGCTCATTTGCCACCCCAAAATGATTGACAGACTCTTATAGAAACACAAAGCCATC
45 TCTTTGAAAGGCTGCATGACCCAGATGTTCTTCTCATACTCTTATGGGGGTGCTGAGATT
TACTGCTGATCTCCATGTCTTGTATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
CCAATCATGAGCGGAAGAAATGTGTGTGGGCTTGTGATACTTTCTGGATTGTGGGCATCT
TCAATGTCTGTAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCAATGAAGT
AGACAGTTTCTTTGTGACCTCCCTTTGGTGATTAACCTTGTCTTGTGTGACACATATATTC
50 TGGGGGTGTTCATGATCTCAACAGTGGCATGATGTCCCTGGTGTGCTTCACTCTCTTGGT
GATCTTCACTACATCATCTGGTCAACGTTCCGCGAGCGTTCCCTTGTGGTGGATCTCCCAA
GCCCTCTCCAGTGCAGTGCCCACTTTACTGTTGTGACCCCTTTTCTTGGGCCATGCACTTT
CATTTATGTGTGGCTTTCAAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
TATACATCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAGAGTCAAGTATTC
55 CATGAGGAACTAAGCAGCCATATCTTTAACTAGGAAGACTGATCATCTCTCTTAA
(SEQ ID NO: 406)

AOLFR218 sequences:

5 METANYTKVTEFVLTLGSLQRETVQLVLFVIFLSFYLFILPGNLIJCTIRLDPHLTSPMYFLLANLA
LLDIWYSSITAPKMLIDFFVERKIIISFGGCLAQFLHFVGASEMFLLIVMAYDRYAICRPLHYA
TIMNRRLCCILVALSWMGFIHSIIQVALIVLRPFCCPNELDSYFCDITQVVRIACANFTPEELVM
ICSSGLSVVCFIALLMSYAFLLALLKXSGSDENTNRAMSTCYSHITIVLMFGPSPSIYIARFDF
SFSLDKVVSVFHTVIFPLLNPIIYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

10 ATGGAACCTGCAAATTACACCAAGGTGACAGAAATTTGTCTCACTGGCCTATCCCAGACTC
GGAGGTCCAACTAGTCTCATTTGTATATTTCTATCCTCTCATTTGTTCACTCCTACCCAGGA
AATATCCTTATCATTTTGCACCATCAGGCTAGACCCCTCATCTGACCTTCTCATGTATTTCTC
GTTGGCTAATCTGGCCCTCCTTGATATTGGTACTCTTCCATTACAGCCCTAAAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGTAT
15 GCTGCTATTCGCCAGCCCTCCACTATGCTACCATCATGAATCGACGCTCTCTGCTGTATCCT
GGTGGCTCTCCTGGATGGGGGGCTTCATTCACTTATAATACAGGTGGCTCTCATTTGTT
CGACTTCTTTCTGTGGGCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTGTG
TCCGGATTGCTGTGCCAACACCTTCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT
GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCCTATGCCCTCTCTGGCCCTGTCTCA
20 AGAAACATTCAGGCTCAGATGAGAATACCAACAGGGCCATGTCACCTGCTATCCCACT
TACCAITGTGGTGCTAATGTTGGGCCATCCATCTACATTTATGCTCGCCCATTTTGACTCAT
TTTCCCTAGATAAAGTGGTGCTGTGTTTCATCTGTAATATTCCTTTACTTAATCCCAT
ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAATAT
ATTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

25

AOLFR219 sequences:

30 MLTSLTDLFCSPIQVAIEKSLPKSMNETNHSRVTEFVLLGLSSRELQPFLLFTLSLLYLAILGNF
LILLTVTSDRLHPTMYFLLANLSEFIDVVCVAFATPKMIADFLVERKTIISFDACLAGIFFVHLFTGS
EMVLLVSMAYDRYVAICKPLHYMTVMSSRRVCVVLVLISWVFGFIHTSQAFTVNLPPCCGN
KLVDSFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVVSYTVILVTVNRSSAMAKAR
STLTAHITVTVLFFGPCIHYVWPFSSYSVDKVLAVFYFTIITLILNPIYTLRNKEVKAAMSKLKS
RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409).

35 ATGCTCACTTCATTAAGTATCTCTGTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT
TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAAATTTGTGTTGCTGGGACTG
TCTAGTTCAAGGGAGCTCCAACCTTTCTTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
TCTGTTGGGCAACTTTCTCATCATCTCACTGTGACCTCAGATTCGCCCTCTCACACCCCA
TGACTTTCTGCTGTGCAAACTGTCAATTAAGACGTATGTGTGCTCTTTTGTCAACCTC
40 AAAATGATTCGACAGACTTTCTGGTIGAGCGCAAGACTATTTCTTTGATGCCCTGCTGGCCC
AGATTTTCTTGTTCATCTCTTCACTGGCAGTGAATGGTGCTCCTAGTTTCCATGCGCCTAT
GACCGTTATGTTGCTATATGCAAACTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
GTGTGTGCTCGTCTCATTTTATGGTTTGTGGGCTCATCCATACTACAGCCAGTTGGCA
TTCATGTTAATCTGCCATTTTGTGGTCTAATAAGGTAGACAGTTTCTTCTGTGACCTTCC
TCTAGTGACCAAGTTAGGCTGCATAGACACTTATGTTGTCACTTACTAATAGTTCGAGAT
45 AGTGAGCTTCTTCTCTGAGTTCCTTTCTCCTCTTGTGCTCCTACACTGTAATACACTTGT
ACAGTTAGGAATGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATGACTGCTCACA
TCACTGTGTCCTTTATTTCTTGGACCATGCAATTTTCACTATGTTGTGGCCCTTCAGCAGT
TACTCAGTTGACAAAGTCTTGTGTAATTTCAACCATCTTCAAGCTTATTTTAAACCTGT
AATCTACACGCTAAGAAACAAGGAAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA
50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTGAGAAACAAGTAA
(SEQ ID NO: 410).

AOLFR220 sequences:

55 MKQYSVGNQHSNYRSLFLPFLCSQMTQLTASGNQTMVTEFLFSMPFHAHRGGLFFIPLLIYG
FILGNLIMFVIQVGMALHTPLVFFISVLSFLEICYTTTTPKMLSLISEQKSIASVAGCLLQMYFF
HSLGITESCVLTAADRYIAICNPLRYPTIMIPKLCIQLTVGSCFCGFLLVLEIAWISTLPFCGS

09886055.062701
102290.5098860

NQIHQIFCDFTPVLSLACTDTFLV VIVDAIHAAEIVASFVIALSYIRIIVILGMHSAEGHHKAFST
CAAHLA VFLFFGSVAVMYLRFSATYSVFDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTACAGTGGGTAATCAACATTTCCAATTATAGGAGTCTCTTGTTTCCCTTTTCT
GTGTTACACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAAATGGTGACTGAGTTCTCT
CTTCTCTATGTGCCGATGCGCACAGAGGTGGCCTCTTATCTTTATTCCCTTGCTCTCTCA
TCTACGGATTATCTCTAACTGGAACCTAATAATGTTTCATTGTCACTCAGGTGGGCATGGC
CCTGCAACACCCCTTTGATTTCTTTATCAGTGTCTCTCTCTCTGGAGATCTGCTATACCA
10 CAACCACCATCCCAAGATGCTGTCTGCTTAATCAGTGAGCAGAGACATTTCCGTGGC
TGCTGTCTCTCTGAGATGTACTTTTCCACTCACTTGGTATCAGAGAAAGCTGTGTCTGC
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAAACCATCA
TGATTCCCAAACCTTTGATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCTCTCTTG
CTTCTGAGATTGCATGGATTTCACCTTGCCTTCTGTGGCTCCAAACAGATCCACCAGAT
15 ATTCTGTGATTTACACCTGTGCTGAGCTTGGCTGACAGATACATTCTAGTGGTCATT
GTGGATGCCATCCATCGAGCGGAAATGTAGCCTCTCTCTGGTTCATTGCTCTATCTCTACA
TCCGGATTATTATAGTATCTGGGAATGCACCTCAGCTGAAAGGTATCAGAAAGCCCTTTTC
CACTGTGCTGTCTCACTTGTCTGTGTTCTTGCTATTTTGGCAGGTTCAGGCTGTGATGATT
TGAGATTCTCAGCCCACTACTCAGTGTGTTGGGACACAGCAATGTGTGCTCACTTTGTGATC
20 TTGCTCCCTTTTCCAAACCCATCATCTATAGCTGAAAAACAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVEFVLVGFPTTPPLQLLLFVLFAYILLTLENALIVFTIWLAPSLHRMPYFYLGH
LSFLELWYINVTIPRLLAAFLTQDGRVSVYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
LTYPSLMPSSLATRLAAASWGSFFSSMMKLLFISQLSYCGPNIINHFFCDISPLLNLTCSDEQA
ELVDLALVLMILLPLAVVSSYTAHAAILRIPTSRGRHKAFSTCAAHLA VVVIYSSSLFTYAR
PRAMYTFNHNKIISVLYTIVPFFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

ATGAGAAATTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCTCCAGCTGCTCTCTTTGTCTTTTGTGCAATTTACCTTCGACATTGTGGAGA
ATGCACTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTC
35 CTGGCCATCTCTCTTCTGGAGCTATGGTACATCAATGTACCACTTCTCGGCTCTTGGC
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCAACATGTACTCT
TTTATTGCTTAGCCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
GGCCATCTGTGGACCCCTCTTTACCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
CTGCTGCCCTTGTGGGCACTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTATTCCCAA
40 TTGCTCATGTGGACCCCAACATTATCAACCACTTTTCTGTGATATTCTCCCACTACTCAA
CCTCACTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCTCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCATTTGGCTGTGGTTTTCATCATACACTGCCATCATGACGCCATCTGAG
GATCCCTACGTCCAGGGGAGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTATCTACTACTCTCTCCACTCTCTTCACTATGACGCGCCCGGGCCATGTACACCTT
45 CAACCAACAACAAGATTATCTGTGCTCTACACTATCATTTGATACCTTCTTCAACCCAGCCA
TCTACTGCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGTATGGGCAGAT
GTCACTACTTAGGATGTTACAGGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQNTVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVLTLSNVFIIAIRLDSHLHTPMYLFSLF
SFSETCYTLGIIPRMLSLGAGGDQAIYSVGCACQMFFSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNPILCAQLVITSFLTGYLFLGMLTVIFHLFSFCSSEHQHFCDDTPPVLSLACGDTGPS
ELRIFILSLVLLVSFFFTITISYAILAAILRIPSAEGQKKAFTCSASHLTVVVIHGYCASVYLRPK
ASYSLERDQLIAMTITVTVTPLLNPIVYSLRTRAIQTALRNAFRGRLLGK (SEQ ID NO: 415).

ATGGGGCAGACCAACGTAACCTCTGGAGGGATTTTGTCTTCTGGGCTTCTCCAGTTCTG
 GGGAGTTGCAGTCTCTTCTTGTGCTTGTTCCTCTCTCTGTATCTAGTCACTCTGACACAG
 AATGTCCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT
 5 CCTTCTCTCTATCTCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAAATGCTCT
 CTGGCTGGCTGGGGGGGACCAGGCTATCTCTATGTGGGCTGTGCTGCCACAGTGTTCCT
 TTCTGGCTCATGGGCTGTACTAACTGCTTCTCTGTGGCTGCCATGGGCTTTGACAGATATG
 TGGCCATCTGTGCTCCACTCCAATATGCCAGCCACATGAATCCACCTCTGTGCCACGT
 GGTCACTACTTCTCTCTGACTGGATACCTCTTTGGACTGGGAATGACACTAGTTATTTTCC
 ACCTCTCATTTCTGCAGCTCCCATGAAATCCAGCACTTTTTTGTGACACGCCACCTGTGCTG
 10 AGCTTCTGAGTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTTATCTCCAGTCTTTGG
 TCTCTTGTGCTCTCTCTTCTTCTATCACCATCTCTCATCGCTACATCTTGGCAGCAATACTG
 AGGATCCCTCTGCTGAGGGGAGAGAAGGCTCTCTCCACTGTGCTCTGCACTTACAGCTTACG
 TGGTCATTATTATTATGGCTGTGCTTCTCTGCTGTAACCTGAGGCCCAAAGCGAGTACTCT
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATCTGTAGTGACCCCTCTTAATCCCA
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEANESSEGISFVLLGLTSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
 20 MEASADLCFASVTVPKMLANLLAHDHSISLAGCLTQMYFFALGVTDSCLLAAMAYDCYVAIR
 HPLPYATRMSRMAALVGMAWLVSHVSHLLYLLMARLSFCASHQVPHFFDHQPLLRLSC
 SDTHHIQLLIFTGGAIAVVVTPFLILASYGAIIAAVALQLPSASGRILAVSTCGSHLAVVSLFYGT
 VIAYVFQATSRREAEWGRVATVMYTVVTPMLNPIIYSLWNRDVQALRALLIGRRISASDS
 (SEQ ID NO: 417).

ATGGAGGCTGCCAATGAGTCTTACAGAGGGAATCTCATTCGTTTTATTGGGACTGACAACAA
 GTCTTGACAGCAGCGGCCCTCTCTTTGTGCTGTCTTGCTCTGTATGTGGCCAGCCTCTGT
 GGTAAATGGACTCATTTGTGGCTGCCATCCAGGCCAGTCCAGCCCTCATGACACCATGACTCT
 TCTGCTGGCCCACTGTCTTTGCTGACCTTGTTTTCGCTCCGCTCACTGTGGCCAAAGATG
 30 TTGGCCAACTTTGTGGCCATGACCACTCCATCTCGCTGGCTGGCTGCTGACCCAAATGT
 ACTTCTCTTTTGCCCTGGGGGTAACATGATAGCTGTCTTGTGGCGGCCATGGCCTATGACTG
 CTACGTGGCCATCGGGACCCCTCCCTATGCCACGAGGATGTCCCGGGCATGTGCGCA
 GCCTGGTGGGAATGGCATGGCTGGTGTCCACGCTCACTCCCTCTGTATATCTGCTCA
 TGGCTCGCTTGTCTTCTGTGCTTCCCAACCAAGTGCCCACTCTTCTGTGACCAACCAAGCT
 35 CTCTTAAGGCTCTCGTGCTGTGACACCCACCACATCCAGCTGCTCATCTTACCAGAGGGCG
 CCCAGTGGTGGTCACTCCCTCTCTGCTCATCTCGCTCTATGGGGCCATCGCAGCTGC
 CGTGCTCAGCTGCCCACAGCTCTGGGAGGCTCCGGCTGTGTCACCTGTGGCTCCCACT
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC
 GAGCGAGGCAGAGTGGGGCCGTGTGCCACTGTGTCATGACACTGTAGTACCCCCATGC
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGCACTCCGAGCCCTTCT
 CATTGGGCGAAGGATCTCAGCTAGTGACTCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

MGSFNTSFEDGFILVGFSDWPQLEPILFVFIIFYSLTLFGNTIIIALSWDLRLHTPMYFFLSHL
 45 LDLCTFTSTVPQLLNLNCVDRTITRGGCVAQLFYIYALGSTCVLLVVMFDRYAAVCRPLHY
 MAIMHPHLQQTILAIASWAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKILACADTEGT
 EAKMFARVIVVAVPAAALILGSYVHIAHVLVKSTAGRRAFGTCGSHLLVFLFYGSJAIT
 YLQSIHNYSEREGKFVALFTTITPILNPLYITLRNKDVKALWKVLWRGRSDS (SEQ ID NO:
 419).

ATGGGAAGTTTCAACACCAAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
 CGCAACTGGAGGCCATCCTGTTGTCTTATTTTATTTTCTACTCCCACTCTTCTTGGC
 AACACCATCATCATCGCTCTCTCTGGCTAGACCTTCGGCTGCACACACATATGTACTTCTT
 TCTCTCTCATCTGTCTCTGACCTCTGCTTCAACACCAAGCAGCTGCCAGCTCTGA
 55 TCAACCTTTGCGGGGTGGACCCACCATCACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCTCGTGTGTGAGGCTTTGACCGCTAT

5 GCTGCTGTCTGTCGTCCTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT
GGCTATCGCCCTCTGGGGTGGCGGTTCTGTAACCTCTGATCCAGACAGGTCTCGCAATG
GCCATGGCTCTCTGTGGCCATCGACTGAACTCACTTCTTGAGATGGCTGTAITTTCTGAA
10 CTGTGGCTTTGTCGGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCGAGTCAATG
CGTGGCTGTTCTGTCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
AGGGTGAAGTCAACCGCTGGGGCGAGAAAGGCTTTTGGGCACTTGTGGGTGCCACCTCTTA
GTAGTTTCTCTTTTATTGGCTCAGCCATCTACACATACTCCAATCCATCCACAATATTTC
TGAGCGTGAGGGAAAAATTTGTTGCCCTTTTTTATACTATAATTACCCCCATTCTCAATCTCT
15 TCATTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

15 MENYNQSTDFILLGLFPSSIIDLFFILIVFIFLMALIGNLSMILLFLDTHLHPMYFLLSQLSLID
LNYISTVTPKMASDFLHGNKSISFTGCCGQSFLLALGGAEALLLSMAYDRYIAICFPLHYLIRM
SKRVCVLMITGWSIIGSINACHTVYVLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYGETV
FLSATIFLVFFPFIGISCSYGVLFAYVYHMKSAEGRKKAYLTCSTHLTVTFYFAPFVYTYLRPRS
LRSPTEKDLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRJCSVKM (SEQ ID NO: 421).

20 ATGGAATAACAATCAACATCAACTGATTTCATCTTATTGGGGCTGTTTCCACCATCAA
TAATTGACCTTTTCTCTCATCTTCATTGTTTCATTTTCTGATGGCTCAATTGGAAACG
TGCCATGATTCTCTCATCTTCTGGACACCCATCTCCACACACCCATGTAITTCCTACTG
AGTCAGCTCTCCCTCATGTACCTAAATACATCTCCACCATTGTTCTCAAGATGGCATCTGA
25 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTCAGATGTTTCTTCT
TGGCATATGAGGAGTGCGAAGCACTACTTTGGCATCTATGGCCTATGATCGTTACATGTC
TATTGCTTTCTCTCCACTATCTCATCCGATGAGCAAAAGTGTGTGCTGCTGATGATA
ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATGTACTCCATA
CTCCTTATGGCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCAGCAATGGTGACT
TTGGCCTGCAATGGACACCTGGGCTCATGAGGGCACAGTGTTTGTGAGCCACCATCTTCT
30 TCGTGTTCCTCTCATTTGGTATTTTCATGTTCTATGGCCAGTTTCTCTTGTCTGTACTACCA
ATAAATCTGCGAAGAGGAGGAAGAAAGCCATTTGACCTGCGACACCCACCTCATGTA
GTAACCTTCTACTATGCACCTTTGTCTACACTATCTACGTCCAAGATCCCTCGGATCTCC
AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCTCTCACCCCAATGCTCAACCCCATC
ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
35 TGCTCTGTGAAATGTAG (SEQ ID NO: 422).

AOLFR226 sequences:

15 MEWRNHSRGSEFVLGFPAPLQVLLFALLLLAYVLVTENTLIIMAIRNHSHTLHKPMYFFL
ANMSFLIEWYVTVTPKMLAGFVGSKQDHGQLISFEGMCTQLYFFLGLGCTECVLLAVMAYD
RYMAICYPLHYPVIVSGRLCVQMAAGSWAGGFISMVKVFLISGLSYCGPNIINHFFCDVSPLL
40 NLCTDMSTAEILDIFILAIFILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLTVVLIF
YAAISIFYARPKALSAFDNTNKLVSPLYAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP
KKASRNV (SEQ ID NO: 423).

45 CTGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTGTGTGCTGGGCTCCCTGCT
CTGCGCCACTACAGGTACTATTGTTGCCCTTTGCTGCTGGCCTATGTTGTTGGCTGAC
TGAGAACACACTCATCATATTAGGCAATTAGGAACCATCTACCCCTCACAAACCCATGTAC
TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATCCCAAGAT
GCTTGCTGGCTTTTGTGGATCCAAACAGGATCATGGACAGCTAATCTCTTGTAGGGATGC
50 ATGACACAGCTCTACTTTTCTTGGCTTGGGCTGCACTGAGTGTGCTCTCTCGCTGTIAT
GGCCTATGATCGCTATATGGCCATCTGCTATCTCTCCACTACCCAGTCAATGTTCAGTGGCC
GGCTGTGTGTGCGAGATGGCTGTGGCTCTTGGGCTGGAGGTTTGGCATCTCCATGGTCAA
AGTTTTCTTATTCTGGCCCTCTTACTGTGCCCAACATCATCAACCATTTTTCTGTG
ATGCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTC
ATCTGGCCATTTTTATTCTTCTAGGGCCACTCTGTGCTGCTGGGCGCTCTTATGTGGCCAT
55 TACTGGTGCTGTGATGCACATATCTCGGCTGCTGGACGCTATAAGGCCCTTTTCCACTGT
GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCACCGAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTA CTGTA CTGCTGTCATTGTA
CCATTGCTCAATCCCATCTATTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCTCGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

AOLFR227 sequences:

MEPQNTSTVTFNQFLLFQGNLLEWQALLFVIFLLIYCLTHGNVVIITVVSQGLRLHSPMYMFLQH
LSFLEVVYTTTVPVLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPFMLMHRGLCARLVVVSWCVTGVTGFLHSMISMISRLDFCGRNGHNHFCDLPLMLQSCSRV
YITEVTIFILSIAVLCICFFLTLGPYVFIWSSILRIPSTSGRRKTFSTCGSHLAVVTLYGYTMISMVY
CPSPHLLPENKIISVYFTVTVPLLPVLIYSLRNKDFKEAVRKVMRRKCGILWTSKRKF
LY (SEQ ID NO: 425).

ATGGAGCCCCAAATACCTCCACTGTGACTAATTTACAGTGTAGGATTCCAGAACCTTC
TTGAATGGCAGGCCCTGCTCTTTGTCACTTTCTGCTCACTACTGCCTGACCAATTATAGGG
AATGTTGTCACTCATCACCCTGGTGAGCCAGGGCTCGCACTGCCTCCCTATGTACATGT
TCCTCCAGCATCTCTCCTTTCTGGAGGTCTGGTACACGTCACCACTGTGCCCTTCTCCTA
GCCAACCTGTGCTCTGGGGCCAAAGCCATCTCCTTCTCTGCCTGCATGGCACAGCTCTACT
TCCTCGTATTCTCTCGGCGCCACCGAGTGCTTTCTCCTGGCCTTCATGGCCATGACCGTTAC
CTGGCCATCTGCAGCCCCATCCGTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGTCTCATGGTGACAGGGGTACGACAGGCTTTCTGCATTCCATGTATGATTTC
AGGTTGGACTTCTGTGGCGCAATCAGATTAAACATTTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCAGAGTTTATATCACCGAGGTGACCATCTTCATCTGTCAATTGCC
GTGCTGTGCAATTGTTTTTTCTGACACTGGGGCCCTATGTTTTCAATTGTGCTCCCATAT
GAGAATCCCTTCCACTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCCACTGGCT
GTTGTCACTCTTACTACGGGACCATGATCTCCATGTATGTGTGTCGACCTGCCCACTGTT
GCCTGAAATCAACAAGATCAITTTCTGTCTTCTACACTGTGGTGACAAACCTGTGAAACCA
GTTATCTACAGCTTGAGGAACAAGACTTCAAGAAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGAGTACAAGTAAAGGAAGTTCTTTATTAG (SEQ ID NO: 426).

AOLFR229 sequences:

MFYVNIQPFQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFAILLLVFTSIASNVVK
IILHIDSRHLTPMPYFLLSLRLDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYTLAGAE
FFLLGLMSCDRYVAICNPLHYPDLMSRKICWLIWAAWLGSGIDGFLLPVTMQPFCASREIN
HFFCEVPALLKLSDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRKRAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTLTPMLNPLIYSLRNKDVGTALQK
VVGRCVSSGKVITF (SEQ ID NO: 427).

ATGTTTATGTAAATCAGATACCTTTCCAACCTTTATCATATCTCTTTCGTGTACCTTACAGA
GCTATGGAGCAGAGCAATATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA
ACGCCGTTTCCCGTGCTTCTTTGCCCTCACTTCTCTGGTCTTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCACTTCTCATCCACATAGACTCCCGCCTCCACACCCCTGTACTTC
CTGCTCAGCCAGCTCTCCTCAGGGACATCTGTATATTTCCACCATGTGCCCAAAATGCT
GGTGACACAGGTGATGAGCCAGAGGCCATTTCTTGTGGTGGTGCAGTGCACCAACTTC
CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTTAGGACTCATGTCTGTGATCGCTA
CGTAGCCATCTGCAACCCCTTGCACTATCTTGACCTCATGAGCCGCAAGATCTGCTGGTGT
ATTGTGCGCGAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCGCTCACCA
TGCAGTTCCTCTTCTGTGCTCTCGGGAGATCAACCACTTCTCTGCGAGGTGCTCGCCCTT
CTGAAGCTCTCTGCAAGCACATCAGCTACGAGACAGCCATGTATGTCTGTGTATTA
TGATGCTCTCATCCCTTCTCTGTGATCTCGGGCTCTTACACAAAGATCTCTACTTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGCAAGGCTGTGGCAACCTGTCTCACACATG
GTGGTTGTGAGCCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATCTTACCA
CACCCCTGAGCAGGCAACAAGCTGTATCTGCCTTCTACACCATCTCACTCCCATGCTCAAT
CCACTCAITTTACAGCCTTAGGAACAAGGATGTACAGGGGGCCCTACAGAAGGTGTGTGGG
AGGTGTGTGCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

AOLFR230 sequences:

MGMEGLLNQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMSDRSLHTPMYFLLS
QLSMDITVYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTLLIGGEFFLLGLMAYDRYVAVCNP
1 5 LRYPLLMNRNRCVLFMVVGSWVWGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPA.VLKLSCDTDS
LYETLMYACCVLMLLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVSVFYGAIFY
TNVLPHSYHTPEKDKVVSFAFYTILTPMLNPLIYSLRNKDVAALRKVLGRGSSQSIRVATVIR
KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTCGTCTCCACAGGCCTCATCACCC
10 ATCCCTGCCCTCCCCGGGCTCTCTTTGCAATAGTCTTCCCATCTTTGGTGGCTATAACA
GCCAACTTGGTCATGATCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT
CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCAAGATGC
TCCAGGACCTCTCTGTCCAAGGACAAGACCATTTCTTCTCTGGGCTGTGCAGTTACAGATCTT
15 CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCTGCTGGGTCTCATGGCCTATGACCGC
TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGTTTGGTTATT
CATGGTGGTGGCTCCTGGGTGGTGGTCTTGGATGGGTTCATGCTGACTCTGTCACT
ATGAGTTTCCCCCTCTGTAGATCCCGAGAGATCAATCACTTTTCTGTGAGATCCCAAGCCGT
GCTGAAGTGTGTCTTGACAGACACGTCACCTCTATGAGACCTGATGTATGGCTGCTGCGTG
20 CTGATGCTGCTTATCCCTCTATCTGTCTCTCTGTCTCCTACACGCACATCTCTCTGACTGT
CCACAGGATGAACCTCTGCTGAGGGCCGGCGCAAAGCCTTGTACGTGTCTCCCAACTT
ATGGTGGTGAGCGTTTCTACGGGGCAGCCTTCTACACCAACGTCGTGCCCACTCTCTACC
ACACTCGAGGAAGAATAAAGTGGTGTCTGCGCTTCTACACCATCTCACCCCACTGCTCAA
CCCCTCATCTACAGCTTGAAGGAATAAAGATGTGGCTGCGACTCTGAGGAAAGTACTAGG
25 GAGATGGTGGTCTCTCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
NO: 430).

AOLFR231 sequences:

MERANHSVSEFILLGLSKSQNLQILFFLGFSVVFVIVLGNLLILVTVTFDSLHLHTPMYFLLSNL
30 SCIDMILASFAITPKMIVDFLRERKTSWWGCYSQMFHMLLGGSEMMMLVAMADRYVAICKP
LHYMTISPRVLTGLLLSSYAVGFVHSSSQMAFMLTLPFCPNVIDSFCDLPVLKACKDITYI
LQLLVIADSGLLSLVCFLLLLVSYGVHFSVRYRAASRSSKAFSTLSAHITVTVTLFAPCVFIYVW
PFSRYSVDKILSVFYTIFTPLNPIIYTLRNQEVKAAIKKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCAGTGGTATCGGAATTTATTTGTTGGGACTTTCAAAATCTC
35 AAAATCTTCAGATTTATTTCTTCTGGGATCTCTGTCTCTGTTGGGATGTTGTTAGGA
AACCTGCTCATCTGGTGACTGTGACCTTTGATTGCTCTCTCACACACCAATGTATTTTCT
GCTTAGCAACCTCTCTGCATGTATGATGATCCTGGCTCTTTTGTACCCCTAAGATGATTG
TAGATTCTCTCCGAGAACGTAAGACCATCTCATGGTGGGGTGTATTCCAGATGTGTTCTT
TATGCACCTCTCGGTGGGAGTGAGATGATGTTGCTTGTAGCATGGCAATAGACAGGTAT
40 GTTGCCATCTGCAAAACCCCTCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC
TACTGTATCTCTCATGTCAGTTGGATTGTGCACTCATCTAGTCAAATGGCTTCATGTGTG
ACTTTGGCCCTCTGTGTGCCAATGTTATAGACAGCTTTTCTGTGACCTTCCCCCTGTGAT
TAAACTTGCTGCAAGGACACCTACATCCTACAGCTCTGTCATTGCTGACAGTGGGCTC
CTGTGACTGGTCTGCTCTCTCTCTCTGCTTGTCTCTATGGAGTCAATAATTTCTCAGTTAG
45 GTACCGTGTCTGTAGTGATCCTCTAAGGCTTTCTCACTCTCTCAGCTCACATCAGAGTTG
TGACTCTGTCTTTGCTCCGTGTGTCTTTATCTACGTCGTGGCCCTTACGACAGATACTCGGTA
GATAAAATCTTCTGTGTTTACACAAATTTACACCTCTCTAAATCTTATTTATTA
ATTAAGAAATCAAGAGGTAAGAGCAGCCATTAAGAAAGACTCTGCATATAA (SEQ ID NO:
432).

AOLFR232 sequences:

MDNITWMASTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
VIFVFLMALSGNAVLLIHCDAHLHTPMYFFISQLSLMDMAYISVTPKMLLDQVMGVNKS
APECGMQMFYVTLAGSEFFLATMAYDRYVAICHPRLYPVLMNHRVCLFLSSGCVFLGSDV
55 GFTFTPTMTFFPFRSREIHFFCEVPAVLNLSCSDSLVEIFMYLCCVLMLLIPVVIHSSSYLLILL

CTCATTGTGACCGTCACCACTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCTCAG
GAATCTGCTATCTTGGATGCCTGCTACATTTCTGTCAGACTCCCTACCTCATGTGCAATT
CCCTACTGGACAGCACCACCATTTCTAAGCGGGATGTGTAGCTCAGGTCTTCTCTCGTGGT
1 TTTTGTGTATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
2 TCTGCCAGCACTTCACTACCTGTGATCGTGAACTCTGAACTCGCATCCAGATGACACT
3 GGCCTCCCTACTCAGTGGTCTGTCTATGCAGGCATGCACACTGGCAGCACAATCCAGCTG
4 NCTGCTCTGCTCCTCAACGTTATTCAATTTCTGTGACATCCCTCTCTGCTGAAGCT
5 CTCTTGCTCTGACACCTTCAGCAATGAGGTGATGATGTTGTCTCTGCTCTGGGGTAGGT
6 GGCGGCTGTTTATCTTTATCATCAGGCTTACATTCACATCTTTCTGACCCGTCTCGGGTT
7 TCCAAGAGGAGCAGACAGAAAGGCTTTTCCACCTGCATCCCTCACATCTCGTGGTGGT
8 TCAGTCTTCTCAGTTCATGCTCTTCTGTGTAACCTCAGGCCACTGCGATACCTGACGCCAC
9 CAGGATCTGATCCTTCTGTTTATTATCCATAAGCTCCCTCTTAAACCCTATTATTTA
10 CAGTCTAGAAATAAGCAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
11 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

AOLFR235 sequences:

MDGVNDSSLQGFVLMGIDHPQLEMIFFAILFSYLLTLLGNSTILLRLEARLHTPMYFFLSNL
SSLDLAFATSSVPMQLINLWPGKTISSYGGCTQLYVFLWLGATECILLVMAFDTRYAVACRPL
RYTAIMNPQLCWLLAVIACLGGGLNSVIQSTFTLQLPLCGHRRVEGLCEVPAMIKLAGCSDTSL
20 NQAVLNGVCTFTTAVPLSIVISYCLIAQAVLKIRSAEGRKAFNTCLSHLLVFLFYGSASYGY
21 LLPAKNSKQDQKGISLFYSLVTPMVNPLIYTLRNMEVKGALRRLGLKGREVG (SEQ ID NO:
22 439).

ATGGACGGGGTGATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
23 CCGAGCTGGAGATGATCTTTTATAGCCATCTCTTCTCCTATTGCTGACCCCTACTGGG
24 AACTCAACCATCATCTTGTCTTCCCGCTGGAGGCCCGGCTCCATACCCATGTACTTCTT
25 CACTAGCAACCTCTCTCTTGGACCTTGTCTTGCCTACTAGTTCAGTCCCAATGCTGA
26 TCAATTTATGGGACAGGCAAGACCATCAGCTATGGTGGCTGCATTAACCCAGCTCTATGT
27 CTTCCTTTGGCTGGGGGCCACCGAGTGCATCTGCTGGTGGTGTGAGCTTTGACCGCTAC
28 TGCGAGTGTGGCGGCCCCCTCCGCTACACCGCCATCATGAACCCCAAGCTCTGCTGGCTG
29 TGCGTGTGATTGCTGCTGGTGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACCT
30 GCAGCTCCCATTTGTGGGCACCGAGGGTGGAGGATTCCTCTGCGAGGTGCCTGCCAT
31 GATCAAACCTGGCTGTGGGCACACAAGTCTCAACCAAGGCTGTGCTCAATGGTGTCTGCAC
32 TTCTTCACTGCAGTCCCACTAAGCATCATCTGATCTCCTACTGCCTCATTTGCTCAGGCAGT
33 GCTGAAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT
34 GCTGGTGGTGTCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
35 AGCAAAACAGGACAGGGCAAGTTCAATTCCTGTCTACTCGTTGGTGCACACCATGGTGA
36 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCATGAGGAGGTGTCTGG
37 GGAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

AOLFR236 sequences:

MTSQERDTAIYSINVSFAKGMTSRSVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
LFLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSFLDACLSTVTPVKVMAGLLTLDGKVIS
FEGCAVQLYCFHFLASTECEFLYTVMAVDRYLAIQPLHYPVAMNRRMCAEMAGITWAGATH
45 AAHTDSLTRLLLYCGPCHIAFYFCDIPPVLKLACTDTTINELVMSIAVGAAGCLILIVISYIFVA
46 AVLRLRTAQGRQAFSPCTAQLTGVLVYVPPVCIYLQPSSEAGAGAPVVFYTVTPMLNPFY
47 TLRNKEVKHALQRLCLSSFRETAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTATTCATTAATGTCAAGTTTGTGTGAAAAG
50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACACAGGAGAACCCCAACAGGA
51 CTGTGGTGAGCCACTTCTTCTGGAGGGTTTGAGGTACACCGCTAAACATCTTAGCCTCTT
52 CTCTCTCTCTTCTCTCATCTACAGCATCACTGTGGCTGGGAATCTCTCATCTCTTAA
53 CTGTGGGCTGACTCTCACCTCAGCTTACCATGTACCACTTCTCTGGGCACTCTCTCTC
54 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTGATGCGAGGCCTGTGACTCTGG
55 ATGGGAAGGTGATCTCTTTGAGGGCTGTGCCGTACAGCTTATTGCTCTCCACTTCTGCG
56 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

- CCCTGCACATCCCGATGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
TGGGCCATAGGTGCCAGGCACGCTGCAATCCACACCTCCCTACCTCCCGCTGCTCTACT
GTGGGCCCTTGGCCACATTGCTACTTCTTCTGCGACATACCCCTGTCTTAAAGCTCGCCTGT
ACAGACACCCACCATTAATGAGCTAGTCTATGCTTGGCAGCATTTGGCATCGTGGCTGCAGGCT
5 GCTTCATCTCTATCGTTAATTCCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
GCCACAGGGCCGGCAGCGGGCTTCTCCCTGCTGCTGCGCAGCTCACTGGGGTGTCTCTGT
ACTACGTGCCACCTGTCTGTATCTACCTGCAGCTCGCTCCAGTGAGGCAGGAGCTGGGGC
CCCTGCTGTCTTCTACACAATCGTAACCTCAATGCTCAACCCATTCACTTACACTTGGCGGA
ACAAGGAGGTGAAGCATGCTCTGCAAGGCTTTGTGCGCAGCTTCCGAGAGTCTACAG
10 CAGGCAGCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

- MDQRNYTRVKEFTFLGHITQSRELSQVLTFLFLVYMTLMGNFLIMVTVTCESHLHPMYFLL
RNLSTILDCFSSTAPKVLIDLLSETKTISFSGCVTQMFFHLLGGADVFLSLVMAFDYRIAISKPL
15 HYMTIMRGRGCTGLIVGFLGGGLVHSLAQISLLPLPVCNPLVDTFYCDVPQVLIKACTDFTT
LELLMISNNGLVSWFVFFLLISYTVILMMLRSHTEGRRKAISTCTSHITVTVLHFVPCIVVYA
RFFTALPTDTAISVFTFVISPLNPIIYTLRNQEMKLAMRKLKRLQGSRILIQ (SEQ ID NO:
443).
- 20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCTGGGAATTACTCAGTCCC
GAGAACTGAGCCAGGTCTTAATTACCTTCTGTTTGTGGTGACATGACAACTCTAATGGG
AAACTTCTCTATCATGTGTTACAGTTACCTGTAATCTACCTTCATACGCCCATGTACTTCC
TGCTCGGCAACCTGTCTATTCTTGACATCTGCTTTCTCTCCATCAGAGCTCTAAGGCTGTG
ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAATATGTTCT
25 TCTTCCACTCTCGGGGGGAGCAGAGCTTTTTCTCTCTGTGATGGCGTTTGACCGGTAT
ATAGCCATCTCCAAGCCCTGCACATATGACCATCATGAGTAGGGGGCGATGACAGGCC
TCATCGTGGGCTTCTGGGTGGGGGGCTGTGCCACTCCATAGCCGATTTCTCTATTGCT
CCCACCTCCTGTGTGGGACCAATGTTCTTGACACTTCTACTGCGATGTCCCCAGGTCC
TCAAACCTGGCTGCACTGACAACTTCACTCTGGAGCTCCTGATGATTTCAATTAATGGGTT
30 AGTCAGTTGGTTGTTATCTTCTTCTCCTCATATCTTACACGGGTCACTCTGATGATGCTGA
GGTCTCACACTGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATACCCG
TGGTGACCTGCAATTCGTGCCCTGCATCTATGTCTAGCCCGGCCCTCACTGCCCTCCCC
ACAGACACTGCCATCTCTGTCACTTCACTGTATCTCCCCCTTGCTCAATCTATAATTGA
35 CACCGTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGAC
AATCAGAAAGGATTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

- MAPENFTRVTEFILTVSSCPQLIPLFLVFLVLYVTMAGNLGHITLSVDSRLQTPMYFRLHL
AINTLNVSTVIAPKMLMNLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP
40 LLYMNVNSTRLLLVSLRLLTYLYGFSTAIYVSPCIFSVYSSNINHVFYCDIAPLLALSCSDTYPI
TIVFISAATNLFFSMITVLVSYFNIVLSILRIRSPGRRKKAFTSCASHMIAVTVFYGTMLFMYLQP
QTNHSLDLDKMAVSFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
445).
- 45 ATGGCTCCTGAAAAATTCACCAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
CAGAGCTCAGATTCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG
GAACCTGGGCATCATCACCCTCACCAGTGTGACTCTCGACTTCAAAACCCCATGTACTTTT
TCTGAGACACTAGCTATCATCAATCTTGGCAACTCTACTGTCACTGCCCTAAAATGCTG
ATGAACCTTTTATGAAGAAAGAAAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG
50 GGTCTGTGTTCTTTATTGTATCGGAGGTAATGATGCTGGGTGATGGCCTATGACCCGTA
TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGGGGGCTCTGCCTCCTGC
TGGTGTCCCTCAGTACCTCTATGGCTTTTCTACAGTATTGTGGTTTACCTTGATATTTCT
TCTGTGCTTATGTCTCTTCTAATAATACATCAATTTTACTGTGATATGGCAGCTCTGTT
AGCAATATCTTGTCTGATACTTACATACAGAAACAATAGTCTTTATATCTGCAGCAACA
55 AATTGTTCTTTTCCATGATTACAGTTCTAGTATCTTAATTTCAATATGTTTGTGCTCACTTA
AGGATACGTTACACAGAAGGAAGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTACACGGTITTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
CACTGGATACGTATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCTCTATGCTGAATCC
CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAAT
CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

5

AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFIFFFGVYVAIMLGNLLILVTISDPLCHSSPMYFLLG
NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQIIFLHFTGGAEMLVLSMAYDRYVAIC
KPLHYMTLMSWQTCIRLVLASVWVGVFVHSISQVAFVNLNYPYCGPNEVDSFFCDLPLVIKLACM
10 DTYVLGHIMISDGLLSLSCFLLLISYTVILLAIRQAAGSTKSALSCSAHIMVVTLLFFGPFIV
YVRPFSRFSDVKLLSVFYIPIPLLNPIYTLRNEEMKAAAMKKLQNRVVTQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTGACAGAAATTTGTTGTGACTGGACTCTGCACCTCAC
GACATCTTCAAAATTTTCTTTATATTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACCTCCCTCATGTACTIT
CCTGCTGGGGAACCTGAGCTTTCTGGACATGTGGCTGGCCTATTTGCCACTCCCAAGAT
ATCAGGGATTTCTCTAGTGATCAAAAACATCATCTCTTTGGAGAGATGTATGGCTCAAAATCT
TCTCTTGCACTTTTCTGGTGGGGCTGAGATGGTGCTCTGTTTCCATGGCCTATGACAG
ATATGTGGCCATATGCAAACCTTGCATTACATGACITTTGATGAGTTGGCAGACTTGCATC
20 AGGCTGGTGCTGGCTTCATGGGCTGTTGGAATTTGTGACTCCATCAGTCAAGTGGCTTCA
CTGTAAATTTGGCTTACTGTGGCCCAATGAGGTAGACAGCTTCTCTGTGACCTCCCTCTG
GTGATCAAACTTGCTGCATGGACACCTATGTCTTGGGTATAATATGATCTCAGACAGTG
GGTGTCTTCTCTGAGCTGTTTCTGCTCCTCCTGATCTCCTACACCGTGATCTCTCGCT
ATCAGACAGCGTGTGCGCGTAGCACATCAAAGCACTCTCCACTTGTCTGACATATGTA
25 TGGTAGTGACGTGTTCTTTGGCCCTTGCATTTTGTATATGTGCGGCTTTGAGTAGTTT
TCTGTGGACAAGCTGCTGTCTGTGTTTATACCATTTTACTCCACTCTGAACCCCATTTAT
CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT
GACTTTTCAATGA (SEQ ID NO: 448).

AOLFR240 sequences:

MAGENHTLPEFLLGFSDLKALQGPLFVWVLLVYLVTLGNSLIILLTQVSPALHSPMYFFLR
QLSVVELFYTTDIVPRTLANLGSHPHQAISFGCAAQMYVIVLGISECCLLTAMAYDRYVAIC
QPLRYSTLLSPRACLAMVGSSWLTHIATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHR
SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTOSRRKVFSTCSSHLLVLSLFFGTASITYRQP
35 AGSSVTTDRVLSLFYVTTPMLNPIYTLRNKDVRRLRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAACCACTACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACTTCTGGG
TAACCTCCTGATCATCTCTCCTCACACAGGTGAGCCCTGACCTCCCATCTGATCTCT
40 TCCCTCGCCCACTCTCAGTGGTGGAGCTTCTTACACCACTGACATCGTGCCAGGACCTT
GGCAATCTGGGCTCCCCGATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCAGATG
TACGTCTCATATGTCTGGGCATCTCGGAGTGCTGCCTGCTCAGGCCATGGCCTATGACC
GATATGTTGGCCATCTGCCAGCCCTACGCTATTCCACCTCTTGAGCCACGGGCTGCTT
GGCCATGGTGGGTCTCTCTGGCTACAGGCATCATCAGGCCACCAACCATGGCTCCCTC
45 ATCTCTCTCTACCTTTTCGAGCCACCCGATCATCCCGCACTTCTCTGTGACATCTGCG
AGTACTGAGGCTGGCAAGTGTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
CATAGTCTTCATTATGATGCCCTTCTCTGTATGTACCTTACATCCGCATCTCGGGTG
CATCTAGCAATGGCCTCCACCCAGAGCGCCGCGCAAGGTCTCTTCCACTTGTCTCTCCA
100 TCTGCTGTGTGCTCTCTCTTTTGAACAGCCAGCATCACTACATCGGCGCGGAGGCA
GGCTCTCTGTGTACCAACAGACCGCGTCTCAGTCTCTTCAACAGTCATCAACCATGCT
CAACCCCATCATCTACACCTTCCGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT
GAAGAGGCAAGCGCCCTCACCTTGA (SEQ ID NO: 450).

AOLFR241 sequences:

MPQILIFTYLNMFYFFPPLQILAEMLTMVTEFLLGFSSLGEIQLALFVVFLLYLVLISGNVTIIS
VIHLDKSLHTPMYFFLGLISTSETFYTFVILPKMLINLLSVARTISFNCALQMFFFLGFAITNCLL

LGVMGYDRIAACHPLHYPTLMSWQVCGKLAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVLLACTNDVNEFVIFCGVLVLVVPFLFICVSYLCILRLIKPSAEGRRKAFSTCAS
HLSVVVHYHGASFIYLRPTANYVSNKDRLVTVTYTIVTPLLNPVVYSLRNKDVQLAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTACTTCTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATCGGTACCGAAATTCCTGTGTGGGTTTTCCAGCCTTGGT
GAAATTCAGCTGGCCCTTTGTAGTTTTCCTTTCTGTATCTAGTCAATCTTAGTGCGCA
TGTGCACATTATCAGTGTCTCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTCC
10 TTGGCATCTCTCAACATCTGAGACCTTCTACACCTTGTCACTTACCCAAAGATGCTCATC
AATCTACTTCTGTGGCCAGGACAATCTCCTCAACTGTGTGCTCTCAAAATGTTCTTCT
CCTTGGTTTTGCCATTACCAACTGCCTGCTATTTGGGTGTGATGGGTATGCGCTATGCTG
CCATTGTGACCCCTCTGCATTACCCCACTCTATGAGCTGGCAGGTGTGTGGAAAACCTGGC
AGCTGCCTGTGCAGTATTTGGTGGCTTCTTGGCCTCTCTACAGTAGTAAATTTAGTTTTCAGCC
15 TCCCTTTTGTAGCGCAACAAAGTCAATCATTACTTGTGACATCTCAGCAGTCATCTT
CTGGCTGTGACCAACAGAGATGTTAACGAATTTGTGATATTCATTGTGGAGTCTCTGTGAC
TTGTGGTTCCCTTCTGTTTATCTGTGTTCTTATCTCTGCACTTCTGAGGATCTCCTGAAG
ATTCCCTCAGCTGAGGGCAGACGGAAGCGTTTCCACCTGCGCCTCTCACTCAGTGTG
TTATGTTTCATTATGGCTGTGCTTCTTCATCTACCTGAGGCCTACAGCAAACTATGTGTCC
20 AACAAAGACAGCGTGGTGACGGTGACATACAGGATGTGCTACCTCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTGGGCAAGAAA
GGTTCTCTAAAACTATATAATTGA (SEQ ID NO: 452).

25

AOLFR242 sequences:

MNTTLFHPYSFELLGPIGLESMHLWVGPPFFAVFLTAVLGNITLFIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTWFTLREISFEGCLTQMFHILCTGMESA VLVAMAYDCYVAICDPLCY
TLVLTKNVSVVMAIAIFLRPLVFVIPFVLFILRLPFCGHQIHPHTYGEHMGRIARLSCASIRVNIYQ
LCAISILVFHIAIVSYVQLCAVLLSSHDARLKAFSTCGSHVCV/MILTFYMPAFFSMTHFRGR
NIPHFHILLANFYVVIPALNSVIYGVRTKQIRAVQLKMFENK (SEQ ID NO: 453).

30

ATGAATACCACTCTATTTTCATCCTTACTCTTCTCTCTCTGGGAATTCCTGGGCTGGAAG
TATGCATCTCTGGGTGTGGTTTTCCTTTCTTGTCTGTGTCCTGACAGCTGTCTTGGGAATA
TCACCATCTCTTTGTGATTACAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTGT
GCCATCTGTGATCATTTGACCCGGGCGCTGTCTACATCCACCATCCCTAAATGCTTGGCAC
35 CTCTGGTTTACCCCTGAGAGAAATCTCCTTTGAAGGATGCCTACCCAGATGTTCTTCATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCCTCTTGTCTACAGTGTGGTGTGACAAACAAGTGGGTGTCAGTGTATGGCA
CTGGCCATCTTCTGAGACCCCTTAGTCTTTGTCAATACCCCTTGTCTATTTATCCTAAGGCT
TCCATTTTGTGGACACCAAAATTTATCCTCATACTTATGGTGAGCACATGGGCATTTGCCCG
40 CTGCTTGTGGCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCTGGT
CTTTGACATCATAGCAATGTGCTTCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCGACGCTAAGGCATTGACGACCTGTGGCTCATGTGTGTGTCATGTT
GACTTCTATATGCTGCTATTTTCTCATTATGACCCATAGGTTTGGTGGGAATATACCTC
ACTTTATCCACATCTCTCTGGCTAATTTCTATGTAGTACATTCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTGAGAACCAACAGATTAGAGCAACAAGTGTGAAAATGTTTTTCAATAAA
AA (SEQ ID NO: 454).

50

AOLFR243 sequences:

MEQVNCITVVREFFVVLGFSSLARLQQLFVIFLLYFLTLGTNAIISTIVLDRALHTPMYFFLAIL
SCSEICYTVFVPMKMLVDLLSQKKTISFLGCAIQMFSFLFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGHGVCMGLMAAACAGGTVSLVTTSLVFHLFFHSSNQLHHFFCDISPLVKLASQHSFG
SQLVIFMLGVFALVIPLLLILVSYRIISAILKIPSSVGRYKTFSTCASHLISVTVHYSCASFIYLRPK
TNYTSSQDTLIGVSYTLTPLFNPIMYSLRNKEFKSALRRITGQTFYPLS (SEQ ID NO: 455).

55

ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTGCTCGCTCTCACTCCCTGGG
CCAGGCTGCAGCAGTGTCTCTTGTATCTCTCTGCTCTCACTGCTCACTCTGGGCACC

1 AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
2 CCTGCCATCCTTTCTTGCTCTGAGATTGTCTATACCTTTGTCAATGTACCCAAGATGCTGG
3 TTGACCTGCTGTCCGAGAAGAAGACCAATTTCTTCTGGGCTGTGCCATCCAATGTTTTC
4 TTTCTTCTTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGCTATGATCGCTATAT
5 GGCCATCTGTAAACCCACTGGCGCTACTCAGTGCTCATGGGACATGGGGTGTGATGTGGACTA
6 ATGGCTGTGCTGCTGTGCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTCTA
7 TCTGCCCTTCACTCCTCCAACCAAGCTCCATCACTTCTCTGTGACATCTCCCTGTGCCTTA
8 AACTGGCATCTCAGACATCCGGCTTCACTCAGCTGGTCATATTCATGCTTGGTGTATTGCG
9 CTGGTCATTCTCTGCTACTTATCCTAGTCTCTACATCCGATCATCTCTGCCATCTAA
10 AAATCCCTTCTCCGTTTGGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTTGTG
11 GTAACCTGTTTCACTACAGATTGTGCCTCTTTCATCTACTTAAAGGCCCAAGACATTAATCACTTC
12 AAGCCAAGACACCCCTAATATCTGTGTCAACACCCTTACCCCATTTGTCAACCTCAAGT
13 ATTTATAGTCTGAGAAATAAGGAAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT
14 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

AOLFR244 sequences:

16 MWQEYYFLNVFFPLKVKVCLTINSHVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSDFTF
17 MGLFNKRETSGLFALISIIFFALTAMANGVMIFLIQTDRLRLHTPMYFLLSHLSLIDMMYISIVPKM
18 LVNYLLDQRTISFVVGTAQHFIYLLTVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI
19 IAGSWFGSLDGLFLLPTMTSPFCNSREINHFFCEAPVLKLCADTALYETVVMYVCCVLMLL
20 IPFSVVLASYARILLTTVQCMSSVEGRKKAFATCSSHMTVVSFLFYGAAMYTYMLPHSYHKPAQ
21 DKVLVSFYTILTPMLNPLIYSLRNKDVGTALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

22 ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCACTTTTAAAGTTTGCTGCCTAAC
23 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
24 TACCTTATATCGGCACAACCTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
25 CACTTTATCGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTGTGCCATCATCTCT
26 ATCATCTTCTTCAACCGCACTGTATGGCCAAATGGGGTTATGATCTTCGTATCCAAACAGATT
27 TGCGCCTTCATACACCCATGTACTTCTCCTCAGCCACCTTTCCTTAATTGACATGATGTAT
28 ATTTCCACTATTGTGCCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCAATTCCTT
29 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCCTCCTG
30 CTGGGCCCTACGGCCTATGACCGCTATGTGGCCATTGTGCAACCTCTGAGATACCCCTGTC
31 TCATGAGCCGCGGGTCTGTGTGGATGATTATAGCAGGTTCTCGTGTGGGGGCTCTTTGGA
32 TGGCTTCTCTGTAACCCCAATCAACATGAGCTTTCCTTCTGCAATTCCCGGGAGATTAAAC
33 ACTTCLDQRTISFVVGTAQHFIYLLTVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI
34 GACAGTGATGTATGTGTGCTGTGTTTGTATGCTGCTGATTCTTCTCTGTAGTCCTTGCTT
35 CCTATGCCCGAATCCTGACTACAGTTCAAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG
36 CATTTGCCACTTGTCTATCCACATGACTGTGGTGTCTTGTCTCAGGGGGCTGCCATGTAC
37 ACCTACATGCTGGCCACTTCTTACCAACAAGCCAGCCAGCAAAAGTCTCTCTGTGTTT
38 ACACCATTTCTACACCCATGCTGAACCCCTCATCTACAGCCTTGAAGAACAAGGATGTGAC
39 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTCAAGGAGGTGT
40 TTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

41 MDLKNGLVTEFILLFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCRSLHSPLYFLLGN
42 LSLFDMCLSTATTPKMIDLLTDHKTISVWGCVTQMFFMHFFGAEMTLLIMAFDRYVAICKP
43 LHYRTIMSKLILKGFALSWIIGFLHSIQVLTMLNPFNGHNVNNIFCDLPLVIKLACIETYILE
44 LFVIADSGLLSFTCFILLVSVYVILVSVPKKSSHGLSKALSTLSAHIVVTLFFGPCIFYVWPFFSL
45 ASNKTLAVFYTVITPLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

50

51 ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
52 GGGAACTTCAAAATTTCTTCTTTGTGACATTTCCCTGATCTACGGTGCTACTGTGATGGGA
53 AACAATCTCATATTGCTGCACAGTGACATGTAGGTCAACCCCTCATCTCCCTGTACTTTCT
54 CCTTGGAAATCTCTCTTTTGGACATGTGTCTCTCCACTGCCACAACCCCAAGATGATCA
55 TAGATTGTCTCACTGACCAACAAGACCATCTCTGTGTGGGGCTGGGTGACCCAGATGTTCTT
56 CATGCACTCTTTGGGGGTGCTGAGATGACTTCTCTGATAATCATGGCCTTGACACGGTAT

GTAGCCATATGTAAACCCCTGCACATATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
TTTGGCATGCTTTTCATGGATAATTGGTTTTTTACACTCCATAAGCCAGATAGTTTTAACAAAT
GAACTTGCCTTTCTGTGGCCACAATGTCATAAAACAACATATTTTGTGATCTTCCCTTGTGA
TCAAGCTTGCTTGCATTGAAACATACACCCCTGGAATTATTTGTGATTTGCTGACAGCGGGCT
5 GCTCTCTTTACCTGTTTCATCCTCTTGCTTGTTCATTACATTGTCATCCTGGTCAGTGTACC
AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCACATCAATTGTG
GTCACCTTGTTCTTTGGACCTTGATTTTTATCTATGTTTGGCCATTCAGTAGTTTGGCAAG
CAATAAAATCTCTGCCGTATTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
10 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT
CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLGLPIRPEQQAVFFTLFLGMYLTTVLGNLLIMLLIQLDLSLHTPMYFFLSH
LALTDISFSSVTPKMLMDMRTRYKSILYEECISQMYFFIFFTDLDSFLITSMAYDRYV AICHPL
HYTVMREELCVFLVAVSWILSCASSLSHTLLLTLSFCAANTIPHVFCDLAALLKLSCDIFLNE
15 LVMFTVGVVVITLPEMCLVSYGYIGATILRVSTPKGIHKALSTCGSHLSVSVLSYGSIFGQYLF
PTVSSSIDKDVIALMYTVVTPMLNPFYISLRNRDMKEALGKLSRATFFSW (SEQ ID NO:
461).

20 ATGAGCCCTGAGAACACAGAGCAGCGTGTCCGAGTTCTCTCTTCTGGGCTCCCCATCCGGC
CAGAGCAGCAGGCTGTGTTCTTACCCCTGTTCTGGGCATGTACTGACCACGGTGTCTGGG
GAACCTGCTCATCATGCTGCTCATCCAGCTGGACATCTACCTTCACACCCCTGTACTCTT
TCTCAGCAGCACTGGCTCTCAGTACATCTCTCTTTTCACTCTGTCATCTCCCTAAGTCTGT
ATGGACATCGCGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
25 TTTTATATTTTTTACTGACCTGGACAGCTTCTTATTACATCAATGGCATATGACCGATAT
GTTGCCATATGTACCCCTCTCCACTACACTGTGTCATGATGAGGGAAGAGCTCTGTGCTTCTT
AGTGCGCTGTATCTTGGATTCTGTCTTGTGGCAGCTCCCTCTCTCACACCTCTCTGCTGACCC
GGCTGTCTTCTGTGTGCGGAACACCAATCCCAATGTCTCTGTGACCTTGTGCGCTGCTC
AAGCTGCTCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTACAGATAGGGGTGGTGG
30 TCAATTACCTGCCATTGATGTTGATCCTGGTATCATATGGCTACATTTGGGCGCCACTCTG
AGGGTCCCTTCACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG
TGGTGTCTCTATTATGGGTCAATATTTGGCCAGTACCTTTTCCGAGCTGTAAGCAGTTCT
ATTGACAAGGATGTCTATTGTGGCTCTCATGTACACGGTGGTCACACCATGTTGAACCCCT
TTATCTACAGCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG
35 CAACATTTTCTCTTGGTGACATCTGACTTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRRPELQIPLFGVFLVIYLTIVVGNLTMIILTKLDSLHHTPMYFSIRHL
ASVDLGNSTVCPKVLANFVDRNTISYYACAAQLAFFLMFIIEFFILSAMAYDRYV AICHNPL
40 YVVMISQRLCHVLVFGQYLYSTFOALMFTIKIFLTFCGSNVISHFYCDDVPLPLMLCSNAQIE
LLSILSFVFNLSSELVLVLSYMLILLAICQMHSAGRKKAFSTCGSHLTVVVVFYGSLLFMYMQ
PNSTHFFDTKMASVFYTLVPLMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAATCTCAAGAGCGGGC
45 CTGAGCTGCAGATTCCTCTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC
AACCTAACTATGATCAATTTGACCAAACTGGACTCCCACTACATACCTATGATCACTTTT
TATCAGACATTTGGCTTCTGTTGATCTTGGAATTTCTACTGTCAATTTGTCCCAAGGTGCTGG
CAAAATTTTGTGTGGGATCGAAATACTATTCTAATTATGCAATGTGCTGCACAGTGGCATCT
TTCCTATTGTTCAATTATCAGTGAATTTTTCATCCTGTGACGCAATGGCCTATGACCCGCTATG
50 GGCCATTGTGAACCCCTCTGCTCTATTATGTTATTATGCTCTCAGCGACTGTGATGATGACTGG
TGGGATTCATAATATCTCTACAGCATTTCAGGCTCTGATGTTCACATTAAGATTTTTTACA
TTGACCTCTGTGGCTCTAATGTGTCATCAGTCATTTTACTGTGATGATGTCTTCTTGTCTACC
TATGCTTTGTCTGAATGCACAGGAATAAGAAATGTGAGCATACTATTTCTGATTTAATTAAT
TGATCTCTCTCTTCTGATAGTCTTAGTGTCTACATGTGATTGTTGTTAGCTATATGTCAA
55 ATGCATCTTCGACAGGACAGGAAAAAGGCTTCTCCACATGTGGTGTCCCAATTTGACAGTGG
TGGTGTGTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTCTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPICALPTGGLLPHPQHTMMEIANVSSPEVFLVLFSTRPSLETVLFIIVLVSYFVMSILNGI
IILVSHDTVHLHTPMYFFLANLPFLDMSFTTISIVPQLLANLVGPKTISYGGCVVQFYISHWL
ATECVLLATMSYDRYAICRPLHYTVIMHPQLCLGLALASWLGGLTSMVGSSTLMLPLCG
NNCIDHFFCEMLIMQLACVDTSLNEMEMYLASFVFFVLPLGLILVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHVAVVSFLFYGSIIFFMYLQPAKSTSHEQKGFALFYTVVTPALNPLIYTLRNTVEKS
ALRHVLENCSSGAGLQAI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
15 GATGGAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCTCCTGGGCTTCTCCACACGA
CCCTCACTAGAAACATGTCCCTTTCATAGTTGTCTTGAGTTTTCATATGGTATCGATCTTGGG
CAATGGCATCATCTATTCTGGCTTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TCTTGGCAACCTCCCCCTTCTGGACATGAGCTTCACCCAGGAGCATGTGCCACAGCTCTCG
GCTAACCTCTGGGGACACAGAAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTCTCAT
20 ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCTGTGGCCACCATGTCTATGACCGCT
ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCTATTATGCATCCACAGCTTTGCCCTTGG
GCTAGCTTTGGCTCCTTGGCTGGGGGGTCTGACCACAGCATGGTGGGCTCCACGGCTCAC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTCTTTTGGAGATGCCCTCA
TTATGCAACTGGCTGTGTGGATACCAAGCTCAATGAGATGGAGATGTACCTGGCCAGCTT
25 TGTCTTTGTGTCTGCCTCTGGGGCTCATCTGTGTCTTACGGCCACATGTGCCCGGCGG
TGTTGAAGATCAGGTACGAGAAGGGCGGAGAAAGGCATTCAACACCTGTCTTCCACAG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTCTACACCGTAGTACCTCTGCGCTG
30 AACCCACTTATTACACCTGAGGAACCGGAGGTGAAGAGGCCCTCCGGCAGCGGATGA
TTAGAGAATGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30 **AOLFR249 sequences:**

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLVLSRLLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIVLLLIYVTSLIGNIMILLIKTDSRLQTPMYFFPHLAFVDICYTSAITPKMLQSFTEEN
35 NLIIFRGCVIQLFVYATFATSDCYLLAIMAMDYVYACKPLRYPMIMSQTVYIQLVAGSYIIGSI
NASVHTGTFISLFCFSKNKINHFFCDGLPILALSCSNIDINILDDVVFVDFDLMTFVIFSYYIM
VTILKMSTAGRKKSFTSCASHLTAVTIFYGTLSSYMLQPQSNNSENKMKVASIFYGTVIPMLN
PLIYSLRNKEKG (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAGTGACTTAAAAATATAGAGCCATTTTATTGCAAAAAAGTC
40 ACAAGGATGTCTCTGCTTTTCTGGGCTCTTCTTGGTCTCTTCTAGACTTTTGGTAGTCAT
GGGTCCAGGAAACAGCACTGAAGTGACTGAATCCATCTCTGGGATTTGGTGTCCAACAC
GAATTTTCAGCATGTCTCTTTCATTGTACTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGAATCCAGACTTCAAAACACCATGATCTTTTTC
45 CACAACATTTGGCTTTTGTGATATCTGTATATCTCTGCTATCACTCCCAAGATGCTCCAA
AGCTTCACAGAAGAAAAATTTGATAACATTTGGGGCTGTGTGATACAAATCTTGATTT
ATGCAACATTTGCAACCACTGACTGTTACCTCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCCCTTCGCTATCCCATGATCATGTCCCAACAGCTCATACCTCAACTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGATACATACAGGTTTTCATCTTCA
50 CTGCTCTTCTGCAAGTCTAATAAAATCAATCACTTTTCTGTGATGTGTCTCCAAATCTTGCT
CCTTTCACTGCTCAACATTTGACATCAACATCATCTAGATGTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTTATGGTCACCATCTGAAG
ATGCTCTTCTACTGCTGGGAGGAAAAATCTCTTCCACATGTGCCCTCCCACTGACAGCAG
TAACCAATTTCTATGGGACACTCTCTTACATGTACTTACCGCTCAGTCTAATAATCTCAG
60 GAGAATATGAAAGTAGCCTCTATATTTATGGCACTGTTATTTCCCATGTGTGAATCCTTTAAT
CTATAGCTTTGAGAAATAAGGAAGGAAAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVLTIGNLLIILAIGSDLHLHTPMYFFLANLSFV
 DMGLTSSVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLSFFLAAMAYDRYVAICHPLCY
 STVMRPQVCALMLALCWVLTNIVALHTFLMARLSFCVTGEIAHFFCDITPVKLKSCSDTHINE
 5 MMVFLVGGTVLIVPFLCIVTSYIHVPAILRVTRGGVGKAFSTCSSHLVCVCFYGTFLFSAYLC
 PPSIASEEKIDIAAAAMYTIVPMLNPFYSLRNKMDMGALKRFLFSHRISVSS (SEQ ID NO: 469).

ATGGAACCAATCCAGCATTTCTGAATTTTCTCCGAGGAATATCAGCGCCTCCAGAGC
 AACACGAGTCCCTCTTCGGAATTTCTCTGTGATGTATCTTGTCACTTGACTGGGAACCTG
 10 CTCATCATCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC
 CAACCTGTCTTTTGTGACATGGGTTAAACGTCTCCACAGTTACCAAGATGCTGGTGAAT
 ATACAGACTCGGCATCACACCATCTCCTATACGGGTGTCCTACGCAAAATGTAATTTCTTTCT
 GATGTTTGGTGATCTAGACAGCTTCTTCTGGCTGCCATGGCGTATGACCGCATGTGGCC
 ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
 15 ATTTGCTGGGTCTCACCAATATCGTGGCTGACTCACACGTTCCTCATGGCTCGGTTGT
 CCTTCTGTGTGACTGGGAAATTGCTCACTTTTCTGTGACATCACTCCTGTCTGAAGCTG
 TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTGTCTTGGGAGGCAACCGTACTCA
 TCGTCCCTTTTATGCATTTGTACCTCCTACATCCACATTGTGCCAGCATCTCTGAGGGTC
 CGAACCCGTGGTGGGGTGGGCAAGGCCTTTCCACCTGCAGTTCCCACTCTGCGTTGTTT
 20 GTGTGTTCTATGGGACCTTCTCAGTGCCTACCTGTGCTCCTCCCTCATGTGCTTGAAGAG
 AAGGACATGACGAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT
 ATAGCTAAGGAACAAGACATGAAGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
 TTGTTTCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

MEGNKTWTDITLPRFQVGPALAILLGLFSAFYTLTLNGVIFIGIICLDCKLHTPMYFFLSHLA
 IVDIYSASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFHVECLILVMSYDRYADWICHPLY
 NILMSWRVCTVLASVWFSFLALVPLVLILRLPFCGPHEINHCEILSVLKLACADTINLQW
 30 VIFAACVFILVGPLCLVLVSYLRLAAILRIQSGEGRRKAFSTCSSHLVCVGLFFGSAIVTYMAPK
 SRHPPEQKQVLSLFYSLFNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTGGTCCCA
 GCACCTGGAGATTCTCCTCTGGGACTTTTCTGCGCTTCTATACACTCACCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCGCTGGACTGTAAGCTTCACACCCCATGTACTTCTCC
 35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAACTATGTCCCAAGATGCTGACG
 AATCTTATGAACCAGGAAGACCATCTCCTTTTTCATGTCATAATGCAGACATCTTGT
 ATTTGGCTTTTGCTCAGTAGAGTGTCTGATTTTGGTGGTGATGTCTATGATCGCTATGGC
 GACATCTGCCAACCCCTTACGTTACAATATCTCATGAGCTGGAGAGTGGCACTGTCTGG
 CTGTGGTCTCTGGGTGTTACGTTCTCTCTGGCTCTGGTCCCTTAGTCTCATCCTGAGG
 40 CTGCGCTTCTGCGGCGCTCATGAAATCAACCACCTCTGTGAAATCCTGTCTGTCCCTCAAGTT
 GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCACTTTTGACGCTGCGTGTTCATCCTG
 GTGGGGCCACTCTGCCTGGTGTGCTGCTTCTTCTGCGCATCTGGCCGCGCATCTGTGAGGA
 TCCAGCTCTGGGAGGGGCCGAGAAAGGCCCTTCTCCACTGCTCTCCCTTCTTGGTGGT
 GGGACTCTTCTTTGGCAGCGCCATTGTACGTAATGGCCCCCAAGTCCCGCCATCTCTGAG
 45 GAGCAGCAGAAAGTTCTTCCCTGTTTTACAGCCTTTTCAATCCAAATGCTGTAACCCCTGA
 TATATAGCCTAAGGAATGCAGAGGTCAAGGGGCGCCTGAGGAGGGCACTGAGGAAGGAG
 AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

MRLANQTLGGDFLLGIFSQISHPGRCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
 IDLTYISVTPVKMLVNLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRYVAICHPLR
 YSVLMHSRVCLLASGCVFVGSVDGFMFLPIAMSPFFCRSHEIQHFCEVPAVLKLKSCSDTSLY
 KIFMYLCCVIMLLIPVTVISVSYYIILTIHKMNSVEGRKKAFTTCSHITVVSFLFYGAAYNYML
 55 PSSYQTPKEDKMSFFYITLTPVLNPIIYFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

ATGCGGCTGGCCAACAGACCCCTGGGTGGTGACTTTTCTCTGTGGGAATCTTCAGCCAGA
 TCTCACACCTGGCCGCTCTGCTTGCATTATCTTCAGTATATTTTGTATGGCTGTGTCTTG
 AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTCTT
 TATAAACACAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTGT
 5 GTGAACCAAGCTGGCCAAAGACAAGACCATCTCGGTCTTGGGTGTGGCCACCAAGATGTAC
 TTCTACCTGCAAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCATGGCCATATGACCGCT
 ATGTGGCTATCTGCCATCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
 CTGGCATCAGGCTGTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATGCCA
 TGAGCTTCCCCTTCTGCAGATCCCATGAGATTGACACTTCTCTGTGAGGTCCCTGCTGTT
 10 TTGAAGCTCTCTTGTCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
 CATGCTCTGTATACCTGTGACGGTCATTTCAAGTGTCTTACTACTATATCTCTCAACCATCC
 ATAAGATGAACACTAGTTGAGGGTCGGAAGAACCTTCAACCATGCTCTCCCATCAATTAC
 AGTGGTCAGCCCTCTTCTATGGAGCTGCTATTACAACATACATGCTCCCCAGCTCCTACCAA
 ACTCCTGAGAAAGATATGATGTCATCCTTTTCTACACTATCCTTACACCTGTCTTGAATCC
 15 TATCATTTACAGTTTCAGGAATAAGGATGTCAAGGGCTTTGAAAAAATGCTGAGCGT
 GCAGAAACCTCCATATTA (SEQ ID NO: 474).

AOLFR253 sequences:

MTFFSSGNCPEVMCSGNQTSQNQTASTDFLTGLFAESKHAALLYTVTFLLFLMALTGNALL
 20 ILIHSEPLRHTPMYFFISQGLALMDLMLYLCVTPKMLVGVQVTDGDTSPSGCGIQMFHLTLAG
 AEFVLLAAMAYDRYAAVCRPLHYPLLMNQVRVQLLVSAWVLMGVLDGLLLTPTMSFFPQCS
 RKILSFFCETPALKLSCDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLHRMNSAAGRRKA
 LATCSSHMIIVLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPVLNPLIYSLRNKDVTAL
 RSMMQSRMNQEK (SEQ ID NO: 475).

ATGACTTTTTTCTCAGGGGGAACACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
 CTCAGAATCAACACAGCAAGCACTGATTTACCCCTACGGGAGCTCTTGCTGAGAGCAAGCA
 TGTGCGCTCTCTACACCGTGACCTTCCCTCTCTTTCTGTGATGGCCCTCATGGGAATGCC
 30 TCTCATCTCTCTCATGCACTCAGAGCCCCGCTCCACACCCCCATGTACTCTTCATCAGC
 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCAAGATGTCTGTGGGCC
 AGGTCACCTGAGAGATGATACCATTTCCCGTCAGGCTGTGGGATCCAGATGTTCTTCCACCT
 GACCTGGCTGGAGCTGAGGTTTCTCTGCTGGCTGCCATGGCCTATGACCATATGACCTGT
 GTTTGCAGACCTCTCCATTACCCACTGCTGATGAACAGAGGGGTGTGCCAGCTCCTGGTGT
 35 CAGCTGCTGGGTTTGGGAATGGTTGATGGTTTGTGTCTACCCCCATTACCATGAGCTT
 CCCCTTTTGCCAGTTAGGAAAAATCCTGAGTTTTTCTGTGAGACTCTCGCCCTGCTGAAGC
 TCTCTGCTCTGACGCTCTCCCTCTATAAGATGCTCAGTACCTGTGCTGCATCCTCATGCTT
 CTCACCCCAATCATGGTCATCTCCAGCTCATACACCTCATCTGCATCTCATCCCAAGGAT
 GAAATCTGCCGCGCCGCCAGGAAGGCCCTGGCCACCTGCTCTCCCATGATCATGATGT
 40 CTGTGCTCTTCCGTTGTCTCTCTACACCTACATGCTCCGAGGTCTTACCAACAGCTGA
 GCAGGACATGATGGTGTCTGCCTTTACACCATCTTCACTCTGTGCTGAACCCCTCATT
 ACAGTCTCCGCAACAAAGATGTCACACGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
 ACAAGAAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

MTNTSSDFTLTLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
 45 MDTLFICTTVPKLLADMVSKKISFVACGIQFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
 VLMNRKKCLLLAAGAWFGSLDGLLTPITMNVPCGSRSNHFFCEIPAVLKACADTSLVET
 LMYICCVLMLLIPISIISTYSYLLTTHRMPSAEGRKKAFTTCSHLLTVVSIFYGAAYFYTVLPQS
 FHTEPQDKVVSIFYTIVTPMLNPLIYSLRNKDVGAFKKVFACSSAQRKVATSDA (SEQ ID NO:
 50 477).

ATGACGAACACATCATCTCTGACTTCACCCCTCTGGGGCTTCTGGTGAACAGTGAGGCTG
 CCGGATTGTATTTACAGTGATCCTTGCTGTTTTCTGGGGGCCGTGACTGCAAAATTGTG
 55 CATGATATTTCTGATTCAGGTGGACTCTCGCTCCACACCCCATGTACTTCTGCTCAGTC
 AGCTGTACATCATGGACACCCCTTTTCATCTGTACCACTGTCCCAAACTCTGGGCAGACAT
 GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTCTTGAGTTCTTCTCCTCTGGGCCCTCATGGCCTATGACTGCTACGTGGCTGT
CTGTAAACCTCTGAGATACCCAGTCTCTGATGAACCGCAAGAAGTGCTCTTTGTGGTGGCTCA
GGTGCTCGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCCACATGAATGTCC
CTTACTGTGGCTCCCGAAGTATCAACCAATTTTTCTGTGAGATCCCAAGCAGTTCTGAAACT
5 GGCCTGTGCAGACACGTCTTGATGAAACTCTGATGACATCTGCTGTGCTCTCATGTGTTG
CTCATCCCCATCTCTATCATCTCCACTTCTACTCCCTCATCTTGTAAACCATCCACCGCAT
GCCCTCTGCTGAAGGTGCAAAAAGGCCCTCACCACTTGTTCCTCCCACTTGACTGTAGTT
AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCAAGTCTTCCACACCCCCG
10 AGCAGGACAAAGTAGTGTGAGCCTTCTATACCATGTGTCAGGCCATGCTTAATCTCTCAT
TCAGCGCTCAGAAACAAGGACGTATAGGGGCAATTAAGGAAGTATTTGCATGTTGCTCA
TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHDSRLHTPMYFLLSQLS
15 REILDILYSTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
YPVLMMSRKICWLVIAAWLGGSIDGFLLPVTMQPFCASREINHFFCEVPALKLSCSTDTSAY
ETAMYVCCIMMLLIPFSVISGYSYTRILITVYRMSEABERGKAVATCSSHMVVVSLFYGAAMYT
YVLPHSYHTEPQDKAVSAFYTLTPMLNPLIYSLRNKDVGTALQKVVGRVCSSGKVTTFF (SEQ
ID NO: 479).

ATGGAGCAGAGCAATTATCCGTGTATGCCGACTTTATCCTTCTGGGTTTGGTTCAGCAACG
CCCGTTTCCCTTGCTTCTCTTGGCCCTCATTTCTCTGGTCTTTTGACCTCCATAGCCAGC
AACGTGGTCAAGATCATTTCTATCCACATAGACTCCCGCTCCACACCCCATGACTTCTCT
25 GCTCAGGCAGTCTCTCCCTCAGGGACATCTGTATATTTCACCAATTGCGCCAAAATGGTG
GTGACCAAGGTGATGAGCCAGAGAGCAATTCTTGTGCTGAGTGCATGCCCAACCACTTCC
TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCTAGGACTCATGTCCTATGATCGCTAC
GTAGCCATTCGCAACCTCTGCATATCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA
TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTGTCAACCCCGTCAACCAT
30 GCAATTCCTCTTCTGTGCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCTCGCCCTTC
TGAAGCTCTCTGACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGATTTAT
GATGCTCTCATCCCTTTCTCTGTCTATCTCGGGCTCTACACAAGAATTCTCATTACTGTTT
ATAGGATGAGCGAGGCAGAGGGGAGGGGAAGGCTGTGGCCACCTGTCTCCACACATGG
TGGTGTGCAGCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCTCATTCTTACCAC
35 ACCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCTTACTCCCATGTCTCAATC
CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGTTGTGGGGGA
GGTGTGTGCTCTCAGGAAGGTAACCACTTCTCAA (SEQ ID NO: 480).

AOLFR256 sequences:

MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLLGNGVIFGIIICLDSKLHTPMYFLLSHL
40 AIDMSYASNNVPMKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVVMYSYDRYVAICHFF
QYTVMSWRVCTILASTCWIISFLMALVHITHILRPFFCGPQKINHFICQIMSFKLACAGPRLNQ
VVLVYAGSAFIVEGPLCLELVSNLHLHLSRHLDPVFMGRAADRLTLPAPSHLCMVGLFGSTMVVM
YMAPKSRHPPEQKVLSLFYSLFNPMNLPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
481).

ATGGGAGGCAAGCAGCCCTGGGTACAGAAATTCATCTGGTGGGATTCCAGGTTGGTGCA
GACTGGCGATTTCTCTCTGTGGACTCTTCTGTCTTCTATACACTCAACCTGCTGGGGGA
TGGGTCATCTTTGGGATATCTGCTGGACTCTAGCTTACACACCCCATGTACTTCTTC
50 TCTCAACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
AAACCTAATGAACACAGAAAGCACCATCTCCTTTGTTCCATGCTAATGCAGACTTTTTTG
TATTTGGCTTTTGTGTTACAGAGTGCCTGATTTGGTGGTGAATGTCCTATGATAGGTATGT
GGCCATCTGCCACCTTTCCAGTACACTGTCTCATCATGAGCTGGAGAGTGTGCACGATCCTG
GCTCAACATCTGGATAAATAGCTTTCTCATGGCTGTGTCATATAACTCATATCTGTAG
60 GCGCGCTTTTGTGGCCCAAAAAGATCAACCACTTTATCTGTCAAACTATGTCGATATCA
AATTGGCTCTGTGTGGCCCTAGGCTCAACCAAGTGGTCTATATGTCGGGTTGCTGGCTCAT
CGTAGAGGGGGCGCTCTGCTGGAGCTGGTCTCCAACCTGCACATCTGTGCGGCCATCTT

AOLFR24B sequences:

MPSINDTHFYPPFFLLGIPGLDTLHIWISPPFCIVYLLAIVGNMILFVIKTEHSLHQPMFYFLAM
LSMIDLGLSTIPKMLGIFWNLQEISFGGCLQMFFIHMFTGMETVLLVVMAYDRFVAICNP
LQYTMILTNKTISILASVVVGRNLVLVTPFVFLRLPFCGHNIVPHITYCEHRGLAGLACAPIKN
IYGLMVISYIIVDVILIASYVLLRAVFLRPSQDVRKAFNTCGSHVCVMLCFYTAFFFSFMTH
RFGQNPYHIHLLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCCTTCATCAATGACACCCACTTCTATCCCCCTTCTTCCTCGTAGGAATACCAGG
ACTGGACACTTTACATATCTGGATTCTTCTCCACTTCTGTATTGTGTACTGATTGCCATTG
TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGCTACACACAGCCCATGTT
CTACTTCTGGCCATGTTGTCTATGATGTGCTGGGTCTGTCCACTCCACTATCCCCAAAA
TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTCAGAT
GTTCTTTATTCACATGTTTACAGGCATGGAGACTGTTCTGTGGTGGTCATGGCTTATGACC
GCTTTGTTGCCATCGCAACCTCTCCAGTACACCATGATCCTCACCATAAAACCATCAG
TATCCTAGCTTCTGTGGTTGTGGAAGAAATTTAGTCTTGTAACCCCATTTGTGTTCTCA
TCTGCGCTTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
TCTGGCCGGTGGCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
TCTATATTTATGTGGATGTGATCTAAATGGCTTCTCCTATGTGCTTATCCTTAGAGCTGT
TTTTGCGCTTCCCTCTCAAGATGTCCGACTAAAGGCCCTCAATACCTGTGGTCTCATGTCT
GTGTTATGCTGTGCTTTTACACACAGCAATTTTTTCTTTATGACACATCGTTTTGGCCAA
AACATCTCCCATATATCCATATTCTTTGGCTAACCTGTATGTGGTGTGCCACCTGCCCT
TAACCTGTTCATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTTGTGAAAATATT
GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

MLHTNNTQFHPSTFLVVGVPGLDVHVWIGFPFFAVYLLALLGNIIILFVIQTEQSLHQPMFYFL
AMLAGTDLGLSTATIPKMLGIFWNLGELIAGFAGCTQMYTIHICTGLESVVLTVTGIDRYAICNP
LRYSMILTNKVIALLGIVIRVTLVFPVTPFTLTLRLPFCGVRIIPHTYCEHMLGLAKACASINCY
GLIAFSVYGIDISVIGFSYVQILRAVFLPAWDARLKALSTCGSHVCVMLAFYLPALFSEFMTHRF
GHNIPHYIHLLANLYVVVPPALNSVIYGVKTKQIREQVRLRLNPKSFWFHDFPKRIFHNNSVRQ
(SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTACCCCTTCCACCTTCTCGTAGTGGGGGTCCCAG
GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCCTTCTTGGCGGTGTATCTAACAGCCCT
TTTACTTCTAGCCATGTGGCCGGCACTGATCTGGGCTGTCTACAGCAACCACTCCCA
AGATGCTGGGAATTTCTGGTTAATCTTGGAGAGATTGCATTTGGTGCCTGCATCACACA
GATGATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
TAGCCATTCTGGGCATAGTCATATTGTGAGGACTTTGGTATTGTGACTCCATTACATTT
CTCACCTGAGATTGCCCTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT
GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTATATATAGGATTGATTGCCCTCTCA
GTGGGATACATTGACATTTCTGTGATTGGATTTCCTATGTCCAGATCCTCCGAGCTGTCTT
CCATCTCCAGCCCTGGGATGCCCGGCTTAAGGCACTCAGCAGCATGTGGCTCTCAGCTGTCT
GTTATGTGGCTTTCTACCTGCCAGCCCTTTTCTTCATGACACACCCGCTTTGGCCAGA
CATCCCTCATACATCCACATCTTCTGTGCCAATCTGTATGTGGTTTTTCCCCCTGCTCTTA
ACTCTGTTATCTATGGGGTCAAAACAAACAGATACAGAGAGGTACTTAGGATACICA
ACCCTAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTCCACAACAATTGAGTATAGACA
ATAA (SEQ ID NO: 490)

AOLFR112B sequences:

MKNKTVLTFEILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILILTLLDSHLQTPMYFFLRNFSF
LEISFTNIFPRVLISITTNKNSISFAGCTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI
MSSRIQICLQFSWLGGLMAIPIITLMSQQDFCASNRLNHYFCDYEPLELSCSDSTSLIEKVVF
VASVTLVVTLLVLSYAFIHKITLKLPSAQQRKAFSTCGSHMIVISLSYSCSMFYINPSAKEG
DTFNKGVALLITSVAPLLNPFHYTLRNQVQKQPFKDMVKLLNL (SEQ ID NO: 491)

5 ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCTGAAC
 TCCAGGTGGCAGTTTTCACCTTCTTTTCTTGGCGTATTACTCAGCATCCTTGGAAATCTG
 ACTATCCTCATCTCACCCTTGCTGGACTCCACCTTCAGACTCCCATGTATTCTTCTCCG
 10 GAACCTTCCCTTCTTGGAAATTTCTTACAAACATCTTCATTCCAAGGGTCTGATTAGCA
 TCACAAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTCTTTGCCAT
 GTTCCTTGGGGCTACAGAGTTTACCTTCTGGCTGCCATGTCCTTATGACCGTATGTGGCC
 ATCTGCAAACTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATT
 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
 15 GGACTTTTGTGCATCCAGACAGACTGAATCATTACTTCTGTGACTATGAGCTCTTCTGGAA
 CTCTCATGTTTCAGACAAGCTCATAGAGAAGGTGTCTTCTGTGGCATCTGTGACCC
 TGGTGGTCACITCGGTGCTAGTGATTCTCTCTATGCATTCAITTAAGCACTATTCTGAAG
 CTCCCCCTCGCCAAACAAAGGACAAAGCCTTTCCACATGTTCTTCCACATGATTGTCA
 CTCCCCTCTTACGGAAGCTGCATGTTTATGTACATTAAATCCCTCTGCAAAAGAGGGAT
 20 ACATTCAACAAGGGAGTAGCTTACTCATTACTTCAGTGTCTCTTGTGTGAACCCCTTAT
 TTACACCCTAAGGAACCAACAGGTAAAAACACCTTCAAGGATATGGTCAAAAGCTTCT
 GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTPSEFHLGDHNLQYLLFTIFFLTYICTLGGNVFIIVTIADSHLHPMYFFLGNL
 ALIDICYTTTNNVQMMVHLLSEKKIISYGGCVTQLFAIFFVFGSECLLLAAMAYDRYIAICKPLR
 YSFIMNKALCSWLAASCSWTCGFLNSVLHTVLTFLHPCFGNNQINVFCDIPLLILSCGDTLSNE
 LALLSIGILISWTFPLCIILSYLYIISTILRIRSSGRHKAFSTCASHLLIVLYYSAIFTYVRPISSYS
 25 LEKDRILISVLVSVPMLNPVIYTLRNKDIKEAVKAIGRWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
 ATGAATTTGCAGTATTACTCTTCACCATCTCTTCTTCTGACCTACATATGCACCTTATAGGAGGC
 AATGTTTTCATTATCTGTGGTGACCATAGCTGATTCACCTACACACACCATGATTATTT
 30 CCTAGGAAATCTTGGCCCTATTGACATCTGCTACACTACTACTAATGTCCCCAGATGATG
 GTGCATTTCTGTGACAGAAGAAATCATTCTATGGAGGCTGTGTGACCCAGCTCTTGT
 CATTCAATTTCTTGTGGCTCAGAGTGTCTCTCTCGGACGAATGGCATATGATCGATAT
 ATTGCTATCTGAAGCCGTTAAGGTACATTTATTATGAACAAGCCCTGTGCACCTGGT
 TAGCAGCTCATGTGGACATGTGGGTTTCTCAACTCAGTGTGTGCACACCGTCTGACCTT
 35 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATATTCTTCTGTGACATACCTCCCTTGC
 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACCTGGCTTGTCTGCCATTGGGATCCCT
 ATAAGCTGGAACCTTTCTGTGCATCATCTTCTTCTACCTTTACATCATCTCCACCATCTCT
 GAGGATCCGCTTCTCTGAGGGGAGGCACAAAGCCTTTCCACCTGTGCTCCCACTGTCT
 40 ATTGTTATTTCTCTATTATGGCAGTGCTATCTTACGTATGTGAGGCCCATCTCATCTTACT
 TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTGTGCACACCATGCTGAATCCT
 GTAATTTATACGCTAAGGAATAAGGACATCAAGAGGCTGTGAAGGCCATAGGAGAGAAAG
 TGGCAGCCACCAGTTTCTCTTCTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQLKMPLFVLFLSIYLFVVGNLGLILLIRADTSLNTPM
 YFFLSNLAVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCLTFMISESLLAMAYDRY
 VAICNPLLYMVVMTPGICQLVAVPYSYSFLMALFHITLTFRLSYCHSNVNHFFYCDMPLRL
 TCSDFTRFKQLWIFACAGIMFISSLLIVFVSYMFIIAISAILRMHSAEGRKQAFSTCGSHMLAVTFYG
 50 TLIFMYLQPSSSHALDTRKMASVFYTVIIPMLNPLYISLQNKVEKALKKIINK (SEQ ID NO:
 495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATCTTGTGG
 GCCTCAGACACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC
 TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATAGAGCGGATACAAGTCTCAACA
 55 CACCAATGTACTCTTCTTAGCAACCTAGCTTTGTGGAATCTTGTTACTCTTCTGTGATT
 ACACCAAAATGCTTGGGAATTTCTTGTACAAACAAATGTTATCTTGTGATGCATGTG
 CTACTCAACTGGGCTGCTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

- GCCTATGACCGATATGTGGCCATTTGTAACCCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCCTTATAGCTATAGCTTCCCTAATGGCACTATTAC
 ACCATCCTCACTTCGCCCTCTCCTATTGCCACTCCAACATTGTCAACCACTTTCTATTGTGA
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 5 GCGCTGTGCTGGTATCAITGTTCAITTCCTCCCTCTGATTGTCTTTGTCTCCTACATGTTTCATC
 ATTTCTGCCATCCTGAGGATGCATTACGTGAGGGAAGACAGAAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCCTCATTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC
 10 CCATGTTGAATCCCTTAATCTATAGCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 AAATCATTATCAATAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

- MAEVNIIYVTVFILKGTNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFDVLCYSSAITPKMMVNFVVERNITPFHACATQLGCLFTFMITECFLLASMAIDCYVAICSPL
 15 HYSTLMSSRRVCQLVAVPYIYSFLVALFHTVITFRLTYCGPNLNHFYCDLPLFALSCLSDTHMK
 EILIFAGFDMISSSSIVLTSYIFHAAILRIRSTQGOHKAISTCGSHMVTVTIFYGLTFMYLQPKS
 NHSLDTKMASVFYTVVIMPLNPLIYSLRNEVKDASKKALDKGCENLQILTFLKIRKLY (SEQ
 ID NO: 497)
- 20 ATGGCTGAAGTTAATATCATTTTATGTCACGTGATTCATTCTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCGTGCTTTGGGGTGTTTATAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTTGATTACTTAAATCAAGATTGATACCTCGACTCCACACCAATGTACTATT
 TCTCAGCCAGCTGCCCTTTGTGACCTTTGTTACTCTCTGCTATTACACCTGAAGATGATG
 GTGAATTTTGTGTGGAAACGCAACACCATTCTTTCATGCTGTGCAACCAACCAAGCGGTT
 25 GTTTTCTCAGCTCATGATCACTGAGTGTTCCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTGCCATCTGTAGTCCCTGCAATTATCAACACTGATGTCAAGAAGAGCTCTGCATTCAAC
 TGGTGCGAGTTCCATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTTC
 TGTGCTGACTACTGTGGCCCAAACCTTAATTAACCATTTCTATTGTGATGACCTCCCTCTT
 AGCTCTGTCTCGCTCAGACACACACATGAAGGAAATTCGATTATTGCTTTTGTGGGCTTT
 30 GATATGATCTCTTCTCTTCCATTGTCTCACTGCTACATCTTATGATTTGCCGCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACAAAGCCATTTCACCTGTGGCTCCCATATGGTGA
 CTGTCACTATTTTCTATGGCACACTGATCTTTATGTACTACAGCCCAAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCATGTGTAACCCCT
 35 TAATCTATAGTCTAAGGAACAAAGAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG
 GTTGTGAAAACCTACAGATATTAACATTTTAAAAATAAGAAAACCTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

- MKNRTMFGEFILLGLTNQPELQVMIFIFLFLTYMLSLGNLTITLTLLDPLHLQTPMYFFLRNFSF
 LEISFTSIFPRFLTSMITGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 40 MSSRVCIQLVFCISWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMVI
 LLAVTVLMTVLVLVLSYTYIIRLIPSAQQRKAFSTCSSHMVISLSYGSCMFMYNPSAKE
 GGAFNKGIAVLITSVTPLLNPFYITLRNQVKQAFKDSVKKIVKL (SEQ ID NO: 499)
- 45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCACTCTTCTGTCTCACCTACATGCTAAGTATCTCTAGGAAATCTG
 ACTATTATCAACCTTCACTTACTAGACCCCCACCTCCAGACCCCCATGATATTCTCTCCCG
 GAATTTCTCCTTCTTAGAAATTTCCCTCACATCCATTTTATTCCAGACTTCTGACAGAGCA
 TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTGTCTAT
 50 ATTTCTTGGAGCTACCGAGTTTACCTCTGGCTCCATGCTCTTATGATCGTTATGTGGCCA
 TCTGCAAAACCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACCTAGTGTT
 CTGCTCTGGTTGGGGGATTCCTAGCAATCTTACCACCAATCTCCTGATGACCCAGGTA
 GATTCTGTGTCTGCAACATCTGAATCACTATTACTGTGACTATGGGCTCTCGTGAGACT
 TGCCTGCTCAGACAACAGCCTCTTAGAATGATGGTCATCTCTTGGCCGTTGTGACTCTC
 55 ATGGTTACTCTGGTGTGCTGGTGGACACTTCTTACACATACATGACTATGAGGACTATTGAGGA
 TCCCTTCTGCCACGCAAGGACAAAGGCCTTTTCCACTTGTTCTCTCCACATGATTGTCTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAACTCCTTCTGCAAAAGAAGGAGGTG
CTTTCAACAAGGAATAGCTGTACTACTTCTGGGTACTCCCTTACTGAATCCCTTCATA
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG
AAACTTTAA (SEQ ID NO: 500)

5

AOLFR274B sequences:

MEFVFLAYPSCPETHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYFLGSLSGIEICYTAV
VVPHILANTLQSEKITTLGTCATQMAFFIALGSDCFLLAAMAYDRYVAICHPLOYPLMLTL
CVHLVVASVISGLFLSLQLVAFIFSLPFCQAQGHFFCDVPPVMHVCAQSHIHEQSVLVAAIL
10 AIAVPFLLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCFAFMLCPSSSYNPKQ
DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATGTTGTCTTCTGGCCTATCCCTCCTGCCAGAACTGCATATTTCTGCTCTTCTTGG
GGTCAGCTGGTGTATTGGTTTGATCATCACTGGGAACATTCTCATTTGTTGGTGTCATTAC
15 ACAGAAACCTGTCTATGCATCCATGTACTATTTCTGGGCAGCCCTTTCTGGGATTTGAAA
TATGCTACACTGCAGTGGTGGTGGCCCATCTCTGGCCAAACCCCTACAGTCAGAGAAGAC
CATCACTCTCTGGCTGTGCCACCCAGATGGCTTTCTTCATTGCAGTGGGCAGTGTGTAT
TGCTTCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTGGCAACCCGTTCAGTA
CCCTCTCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
20 TGTCTCTGTCTTACAACTGGTGGCCTTCATCTTCTCTGCCATTCTGCCAGGCTCAGGGC
ATTGAGCACTTCTTTGTGATGTGCCACCACTGCATGTTGTTGTGTCAGAGTCACAT
TCATGAGCAGTCAGTGTCTGGTGGCAGCCATACAGCAATTGCTGTGCCCTTCTTCTCTCAT
ACCACCTCTACACTCTCATAGTGGCTGCTCTGTCAAGATCCACTCAGTCAGTGGCCGCC
ACCGGGCCCTTCTCACTGTCTTCCCACTCACTGTGGTGTGCTGCGATATGGCTGCTGT
25 GCCTTCATGTACTGTGCCAGCTCCAGTCAACCCCAAGCAAGTCGGTTCATCTCAT
TGGTGTACACATTGGGAACCCCACTGCTCAACCCACTTATCTATGCCCTTGAGGAACAGTGA
GATGAAAGGGCCCTAGGGAGAGTTCCTACCAGGAACCTGCCTTCTCCAGAACAGCTAG
(SEQ ID NO: 502)

AOLFR276B sequences:

MGGFGTNISSSTSFLLTGFPMEKGLEHWLAALLLLLYAISFLGNILIFIIKEQSLHQPMYYFLS
LFSVNDLGVSFSTLPTVLAACVCFHAPETTFDACLAQMFHIFSSWTEFGILLAMSFHDHYVAICNP
LRYATVLDYRVVAHNGISIVIRSFVFLPLFLKRLPFCKASVLAHSYCLHADLIRLPWGD
TINSMYGLFIVISAFGVDSLLILSYVLILHSVLAIASRGERLKLNTLNCVSHIYAVLIFYVPMVSVS
30 MVHFRGHRHAPYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTATGCTATTTCCTT
30 CCTGGGCAACCTCTCATCTCTTATCATAAAGGAAGAGCAGAGCTTGACACGACCAATG
TACTACTTCTGTCTCTTTTCTGTGTAATGACCTGGGTGTGCTCTTCTACATTGCCCACT
GTACTGGCTGCTGTGTTTCATGCCCCAGAGACAACTTTGATGCCTGCTGCTGGCCAGAG
TGTTCTTATCCACTTTTCTCTGGACAGAGTGTGCCATCTACTGCCCATGAGTTTTCAG
CACTATGTCGCCTCTGTGAACCCGCTGCGCTATGGCAAGTGCCTCACTGATGTCGGTGTGG
45 CCCACAATGGCATATCCATTGTCTATCGCAGCTTCTGCAATGGAATCCCACTTCCCTTCTCT
CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCCATCTCACTGCTTGCATG
CAGACCTGATTCGGCTGCCCTGGGGAGACACTACCATCAACAGCATGATGGCTGCTTCAT
TGTCATCTCTGCTCTTTGGTGTAGATTCACTGCTCATCTCTCTCTCTATGTGCTCATTTCTAC
ATTCTGTGCTGGCCATTGCCCTCAGGGGGTGAGAGGCTTAAGACACTCAACACATGCTGGTGC
ACATATCTATGCAAGTGCATCTTCTATGTGCCATATGGTTAGTGTGTCATGGTTCATCGAT
50 TTGGGAGGCATGCTCTGAAATATGTGCACAAGTTTCATGCTCTTTGTACCTCCAATGCTCT
ACCAATTATCTATCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

MDWENCSSLTDFPLLGITNPNEMKVTLFAVFLAVYIINFANLGMIVLIRMDYQLHTPMYFFLS
HLSFCDLVCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLLSVMAFDRIYKAIINP
55 LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFPGSNEINHFFCDIPPLLLSRSDTQV

NELVLTFTVFGFIELSTISGVFISYCYIILSVLEIHS AEGRFKALSTCTSHLSAV AIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKLKNKILF (SEQ ID NO: 505)

ATGGACTGGGAAAAATGGCTCCTCATTAAGTATTTTCTCTTGGGAATTACCAATAACCC
5 AGAGATGGAAGTGACCTATTGGCTGATTCTTGGCTGTTTATATCATTAATTTCTACGAA
ATCTTGGGAATGATAGTTTAAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCT
CCTCAGTCATCTGCTCTTCTGTGATCTCTGCTATTTCTACTGCAACTGGGCCCCAAGATGGCTGG
TAGATCTACTTGGCCAAAGAACAAAGTCAATACCCCTCTATGGCTGTGCTGTGCAATTTCTGGT
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTCAGTGATGGCCTTTGATCGGTACA
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAAATCATTTCTCTGTGATATCCCTCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTIAGTGTATATCACCGCTCTTGGTTTAA
TTGAACTGAGTACCAATTTCAAGAGTTTCAATTTCTATTGTTATATCATCCTATCAGTCTTG
15 GAGATACACTCTGTGAGGGGAGGTTCAAAGCTCTCTCATACGCACTTCCCACTTATCTG
CGGTGCAATTTTCCAGGGAACCTCTGCTCTTATGTATTTCCGGCCCAAGTTCTTCATATCT
CTAGATCAAAGATAAAATGACCTCAATTGTTTTACACCCCTGTGGTTCCTGTTGAACCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAAGTAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

20

AOLFR314 sequences:

MEVKNCCMVTEFILLPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVNDMGFSVTPCKMLLYLMLGSLRLSYKDCVCQLFFHFLGSIIEFLFTVMAFYDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCIHSILSLTFLTPYCGPNEVDHFFCDIPALLACADTSL
25 AQRVSFTNVNGLSLVCFLLILLSYTRITISILSIRTTEGRRRAFTCAASHLAILCAGPIITVYLGPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHPVES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTACCTTTTGGGAATCCCACACACA
30 GAGGGGCTGGAGATGACACTTTTGTCTTATCTTGCCTTCTATGCCTGCACCTCTACTGGG
AAATGTGTCTATCCTGTGTGTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT
TCTGGGAAAGCTTGCTGTGTGTGACATGGGTTTCTCTCAGTGACCTGTGCCAAAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCCTCGGGAGCATTGAGTGCTTCTGTGTTACGGTGATGGCCTATGACCGCTTC
35 ACTGCCATCTGTATCCTCTGCGATACACAGTCATCATGAACCAAGGATCTGTGTGGCCC
TGGCTGTGGGCACATGGCTGTAGGGTGCAATTCATTCAGATCTTGACCTCCCTCACTTC
ACCTTGCCATCTGTGTGCCCAATGAAGTGGATCACTTCTCTGTGATCACTCCAGCAGCTGT
GCCCTTGGCCTGTGTGACACATCCTTAGCCAGAGGGTGAGCTTCAACACGTTGGCCTC
ATATCTTGTCTGCTTTCTGCTAATCTTTTATCCTACACTAGAATCAACAATATCTATCTT
AAGCATTCGTACAACGTAGGGGCCGTGCGCGTGCTTCTCCACCTGCAGTGCTCACTCATTT
40 GCCATCTCTGTGCTATGGGCCCATCATCACTGCTACTGCGAGCCCAACCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAAGCCCTGAAAAACAATATGCACAGGACAGG
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

AOLFR324B sequences:

MPIANDTQFHTSSFLLGIPGLEDVHIWIGFPFFSVYLIALLGNAIFFVIQTEQSLHEPMMYCLA
MLDSIDLSLSTATIPKMLGIFWFIKIEISFGGYLSQMFFIHFVTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKISLIAGIAVLRSLYVMVPLVFLLLRLPFCGHRIPHTYCEHMGARLACASIKVNM
FGLGSISLLLLDVLILSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
50 DIPQYIHIFLANLYVVVPTPLNPLVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCACATCTTCTCATTCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACACTCGGATTGGATTCCCTTTTCTGTGTGATCTTATTGTCACTCC
TGCGAAATGCTGCTATCTCTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTA
55 CTACTGCTGGCCATGTGGATTCCATTGACCTGAGCTGTCTACGGCCACCATTCCTCAA
ATGCTGGGCATCTCTGGTTCAATATCAAGAAATATCTTTGGAGGCTACCTTCTCAGA

5 TGTTCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
CGCTACATTGCCATTTGCAAACTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
GCCTCATTCGAGGCATTGCTGTCCTGAGGAGCTTGATACATGGTCATTCCACTGGTGTCTTC
CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
GCATTGCCCGCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
10 TTTCTCTTGTGTTATTTGGATGTGCTCCTTATATTTCTCTCCCATATCAGGATCCTCTATGCTGT
CTTCTGCGTGGCCCTCTGGGAAAGCTCGACTCAAAGCTCTAACACCTGTGGCTCTCACATT
GGTGTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTCTTTACACACTGCTTTGGCCAT
GATATTTCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTTCTCTCCCACTCT
CAATCTCTGAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC
TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

15 MALGNHSTITEFLLGLSADPNIRALLFVFLGIYLLTIMENLMILLVIRADSLHKPMYFFLSH
LSFVDLCFSSVIPMKLENLLSQRKTISVEGCLAQVFFVFVTAGTEACLLSGMAYDRHAAIRRP
LLYGQIMGKQLYMHLVWGSWGLGFLDALINVLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDI
SRSLIVLLCSTLLHGLGNFLLVFLSYTRIIISTISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
MPNSGSPIELFISVQYTVTPMLNSLIYSLKNKEVKVALKRTLEKYLYQYTR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATACCGAGTTCCTCTCTCTGGGCTGCTGCGCGACC
CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTGGGGATTACCTCCTGACCATAATGGA
AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCCTGTCTCCATAAGCCCATGTATTTCT
TCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTCAGTCATTGTGCCCAAGATGCTG
25 GAGAACCTCTCTGCACAGAGGAAAACCATTTCACTAGAGGGCTGCCTGGCTCAGGTCTTCT
TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
TGCTGCCATCCGCCGCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCTCTAGCTG
TAAACATGGTCTTTTGTGAAGCCAAAATCATTCACCACTACAGCTATGAGATGCCATCCCT
CCTCCCTCTGTCTGCTCTGATATCTCCAGAAGCCTCATCGTTTGTCTGTCTCCACTCTCC
30 TACATGGGCTGGGAACTTCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCATCCATC
CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCACCTCA
CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCCGCCATCTCATGCCAACTCAGGTTT
CCCCATAGAGTTGATCTTCTGTGTCAGTATAGCTAGTCACTCCCATGCTGAATTCCTCA
TCTATAGCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAAGAACTTTGGAAAAATATT
35 TGCAATATACCAGACGTGA (SEQ ID NO: 512)